

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 26, 2005, 01:06:48 ; Search time 519 Seconds
(without alignments)
680.784 Million cell updates/sec

Title: US-10-666-642-194_COPY_111_164

Perfect score: 298

Sequence: 1 DGFPRKRYKKSVQNKINR.....RVERGDGDAAYVITYGVGH 54

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7331713 seqs, 3271544945 residues

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=nrnp -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blousem62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10666642@cgn1.1.798 @runat_25082005_130057_24954
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Published Applications NA:**
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
 - 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
 - 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
 - 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
 - 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
 - 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
 - 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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 - 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
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 - 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
 - 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
 - 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
 - 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
 - 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	100.0	585	18	US-10-412-699B-805
2	249	83.6	641	18	US-10-425-114-12391
3	249	83.6	823	18	US-10-412-699B-1614
4	249	83.6	880	19	US-10-767-701-11768
5	249	83.6	1039	20	US-10-425-115-73408
6	249	83.6	1663	17	US-10-374-780A-1531
7	249	83.6	1663	18	US-10-412-699B-1621
8	248	83.2	680	18	US-10-412-699B-1613
9	248	83.2	743	18	US-10-412-699B-1612
10	248	83.2	802	20	US-10-425-115-93169
11	247	82.9	666	19	US-10-437-963-63714
12	247	82.9	952	18	US-10-425-114-10354
13	247	82.9	974	18	US-10-424-599-115917
14	247	82.9	974	18	US-10-412-699B-1609
15	244	81.9	580	20	US-10-425-115-74300
16	244	81.9	1696	17	US-10-374-780A-1530
17	244	81.9	1696	18	US-10-412-699B-1620
18	243	81.5	669	19	US-10-767-701-1686
19	243	81.5	834	18	US-10-412-699B-1615
20	243	81.5	834	20	US-10-425-115-90976
21	242	81.2	352	20	US-10-856-499-1204
22	242	81.2	603	20	US-10-425-115-132529
23	242	81.2	821	19	US-10-437-963-77029
24	242	81.2	825	17	US-10-374-780A-1529
25	242	81.2	825	18	US-10-412-699B-1616
26	242	81.2	961	19	US-10-437-963-55249
27	242	81.2	999	20	US-10-425-115-170166
28	239	80.2	1235	18	US-10-424-599-112793
29	239	80.2	1235	18	US-10-412-699B-1608
30	237	79.5	1120	19	US-10-437-963-34431
31	232	77.9	999	17	US-10-374-780A-1532
32	232	77.9	999	18	US-10-412-699B-1622
33	232	77.9	1092	19	US-10-437-963-31295
34	230	77.2	748	10	US-09-533-029-29
35	230	77.2	748	10	US-09-534-455-195
36	230	77.2	748	17	US-10-225-066A-1
37	230	77.2	748	17	US-10-374-780A-253
38	230	77.2	748	18	US-10-412-699B-807
39	230	77.2	748	22	US-10-225-066A-1
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41	197	66.1	724	10	US-09-533-029-15
42	197	66.1	724	14	US-10-278-173-63
43	197	66.1	724	18	US-10-412-699B-85
44	197	66.1	1306	17	US-10-225-066A-1033
45	197	66.1	1306	17	US-10-374-780A-2611

ALIGNMENTS

RESULT 1
US-10-412-699B-805
; Sequence 805, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Broun, Pierre E.
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-Liang

```
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: DuBell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kumimoto, Roderick
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142
; PRIOR FILING DATE: 2001-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 805
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1274
US-10-412-699B-805

Alignment Scores:
Pred. No.: 7,258-35 Length: 585
Score: 238.00 Matches: 54
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-412-699B-805 (1-585)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20
331 GATGGTTTAAATGAGGAGGATGCGAAGAAATCTGTCAAAACCAACATTAAACAAGG 390

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
391 AATTACTACAAATGCTCAAGTGAAGGTTCTCGGTGAAGAAGAGGGTAGAGAGATGTT 450

QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
451 GACGATGCAGCTTATGTAATTAACATATGAGGATCCAT 492

RESULT 2
US-10-425-114-12391
; Sequence 12391, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12391
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701174191_FLI
US-10-425-114-12391

Alignment Scores:
Pred. No.: 2,02e-27 Length: 641
Score: 249.00 Matches: 44
Percent Similarity: 88.89% Conservativeness: 4
Best Local Similarity: 81.48% Mismatches: 6
Query Match: 83.56% Indels: 0
DB: 18 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-425-114-12391 (1-641)

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106 GACGGATTCAAGTGGAGGAAGTACGGGAAGAAGCCGCTCAAGAAGACAGCCCAATCCAAGG 165

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
166 AACTACTACCGCTGCTCGTGGAGGGCTGCGGCTGAAGAAGCGGTGGAGAGGACCGC 225

QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
226 GACGACCCCGCTACGTACATCAACCCTACGACGCGGTCCAC 267

RESULT 3
US-10-412-699B-1614
; Sequence 1614, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Broun, Pierre E.
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: DuBell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kumimoto, Roderick
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
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OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS16930 1

; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James E
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1531
; LENGTH: 1663
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Predicted polypeptide sequence is orthologous to G1275
US-10-374-780A-1531

Alignment Scores:
Pred. No.: 7,35e-27 Length: 1663
Score: 249.00 Matches: 44
Percent Similarity: 88.89% Conservative: 4
Best Local Similarity: 81.48% Mismatches: 6
Query Match: 83.56% Indels: 0
DB: 17 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-374-780A-1531 (1-1663)

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QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysArgValGluArgAspGly 40
DB 1138 AACTACTACCGTCTGCTCGAGGGCTGCGCGGTGAAGACGGGTGGAGAGGACCGC 1197
QY 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
DB 1198 GACGACCCCGCTACGTCTATCATCCACCTACGACGGCGTCCAC 1239

RESULT 7

US-10-412-699B-1621

; Sequence 1621, Application US/10412699B

Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Broun, Pierre E.
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James S.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: DuBell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kumimoto, Roderick
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142
; PRIOR FILING DATE: 2001-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1621
; LENGTH: 1663
; TYPE: DNA
; ORGANISM: Zea mays
US-10-412-699B-1621
Alignment Scores:
Pred. No.: 7,35e-27 Length: 1663
Score: 249.00 Matches: 44
Percent Similarity: 88.89% Conservative: 4
Best Local Similarity: 81.48% Mismatches: 6
Query Match: 83.56% Indels: 0
DB: 18 Gaps: 0
US-10-666-642-194_COPY_111_164 (1-54) x US-10-412-699B-1621 (1-1663)
QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAlaAsnLysArg 20
DB 1078 GACGGATTCAAGTGGAGGAAGTACCGGAAGAGCGCGTCAAGAACAGCCCAATCCAAAGG 1137
QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysArgValGluArgAspGly 40
DB 1138 AACTACTACCGTCTGCTCGAGGGCTGCGCGGTGAAGACGGGTGGAGAGGACCGC 1197
QY 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54

Db 1198 GACGACCCCCCTAGCTCATCCACCTACGACGGCTCCAC 1239

RESULT 8

US-10-412-699B-1613

; Sequence 1613, Application US/10412699B

; Publication No. US20040045049A1

; GENERAL INFORMATION:

; APPLICANT: Mendel Biotechnology, Inc.

; APPLICANT: Zhang, James

; APPLICANT: Fromm, Michael E.

; APPLICANT: Heard, Jacqueline E.

; APPLICANT: Riechmann, Jose Luis

; APPLICANT: Adam, Luc J.

; APPLICANT: Broun, Pierre E.

; APPLICANT: Reuber, T. Lynne

; APPLICANT: Keddle, James S.

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Jiang, Cai-Zhong

; APPLICANT: Samaha, Raymond R.

; APPLICANT: Pilgrim, Marsha L.

; APPLICANT: Creelman, Robert A.

; APPLICANT: DuBell, Arnold N.

; APPLICANT: Ratcliffe, Oliver

; APPLICANT: Kumimoto, Roderick

; APPLICANT: Sherman, Bradley K.

; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants

; CURRENT APPLICATION NUMBER: US/10/412,699B

; PRIOR FILING DATE: 2003-04-10

; PRIOR APPLICATION NUMBER: 09/394,519

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: 09/489,376

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: 09/506,720

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: 09/533,030

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,392

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,029

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/532,591

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,648

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/713,994

; PRIOR FILING DATE: 2000-11-16

; PRIOR APPLICATION NUMBER: 09/819,142

; PRIOR FILING DATE: 2001-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 2011

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1613.

; LENGTH: 680

; TYPE: DNA

; ORGANISM: Zea mays

US-10-412-699B-1613

Alignment Scores:

Pred. No.: 3,1e-27

Score: 248.00

Percent Similarity: 92.59%

Best Local Similarity: 77.78%

Query Match: 83.22%

DB: 18

Length: 680

Matches: 42

Conservative: 8

Mismatches: 4

Indels: 0

Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-412-699B-1613 (1-680)

Qy 1 AspGlyPheLysTrpArgLysSerValLysAsnAsnLysArg 20

Db 57 GACGGCTAAGTGGAGGAGTACGCGTCAAGAACACGCCCAACCAAGG 116

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40

Db 117 AACTACTACCGTCTCGACGGAAGGGTGCACGTCGAAGAGCGGTGGAGCGGACCAAG 176

Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54

Db 177 GACGACCCCGCTACGCTGGTGGACGACGTCACGAGGGGATGCAC 218

RESULT 9

US-10-412-699B-1612

; Sequence 1612, Application US/10412699B

; Publication No. US20040045049A1

; GENERAL INFORMATION:

; APPLICANT: Mendel Biotechnology, Inc.

; APPLICANT: Zhang, James

; APPLICANT: Fromm, Michael E.

; APPLICANT: Heard, Jacqueline E.

; APPLICANT: Riechmann, Jose Luis

; APPLICANT: Adam, Luc J.

; APPLICANT: Broun, Pierre E.

; APPLICANT: Pineda, Omaira

; APPLICANT: Reuber, T. Lynne

; APPLICANT: Keddle, James S.

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Jiang, Cai-Zhong

; APPLICANT: Samaha, Raymond R.

; APPLICANT: Pilgrim, Marsha L.

; APPLICANT: Creelman, Robert A.

; APPLICANT: DuBell, Arnold N.

; APPLICANT: Ratcliffe, Oliver

; APPLICANT: Kumimoto, Roderick

; APPLICANT: Sherman, Bradley K.

; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants

; CURRENT APPLICATION NUMBER: US/10/412,699B

; PRIOR FILING DATE: 2003-04-10

; PRIOR APPLICATION NUMBER: 09/394,519

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: 09/489,376

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: 09/506,720

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: 09/533,030

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,392

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,029

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/532,591

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/533,648

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 09/713,994

; PRIOR FILING DATE: 2000-11-16

; PRIOR APPLICATION NUMBER: 09/819,142

; PRIOR FILING DATE: 2001-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 2011

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1612

; LENGTH: 743

; TYPE: DNA

; ORGANISM: Zea mays

US-10-412-699B-1612

Alignment Scores:

Pred. No.: 3,49e-27

Score: 248.00

Percent Similarity: 92.59%

Best Local Similarity: 77.78%

Query Match: 83.22%

DB: 18

Length: 743

Matches: 42

Conservative: 8

Mismatches: 4

Indels: 0

Gaps: 0

Db 376 GATGATCAAGTCGAGGAGTACGGCAGAAAGTCCGCGAAGAGCAGTCCCAATCTAAGG 435
Qy 21 AsnTyTrtYrLysCysSerSxerGluGlyCysSerVallysLysArgValGluArgAspGly 40
Db 436 AACTACTACAAATGTTCAAGTGGAGGATGCGAGTGTGAAGAAAGGGTGGAAAGGGATAGA 495
Qy 41 AspAspAlaAlaTyTrValIleThrTyTrGluGlyValHis 54
Db 496 GATGACTACAGCTACGTCATCAACATATGATGAAGGTGTGCAC 537
RESULT 13
US-10-424-599-115917
; Sequence 115917, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 115917
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_75684C.1
US-10-424-599-115917
Alignment Scores:
Pred. No.: 7,13e-27 Length: 974
Score: 247.00 Matches: 45
Percent Similarity: 90.74% Conservative: 4
Best Local Similarity: 83.33% Mismatches: 5
Query Match: 82.89% Indels: 0
DB: 18 Gaps: 0
US-10-666-642-194_COPY_111_164 (1-54) x US-10-424-599-115917 (1-974)
Qy 1 AspGlyPheLysTrpArgLysTyTrGlyLysSerVallysAsnAenIleAsnLysArg 20
Db 393 GATGGATACAAAGTCGAGGAGTACGGCAAGAGTCCGCGAAGAGCAGTCCCAATCTAAGG 452
Qy 21 AsnTyTrtYrLysCysSerSxerGluGlyCysSerVallysLysArgValGluArgAspGly 40
Db 453 AACTACTACAAATGTTCAAGTGGAGGATGCGAGTGTGAAGAAAGGGTGGAAAGGGATAGA 512
Qy 41 AspAspAlaAlaTyTrValIleThrTyTrGluGlyValHis 54
Db 513 GATGACTACAGCTACGTCATCAACATATGATGAAGGTGTGCAC 554
RESULT 14
US-10-412-699B-1609/c
; Sequence 1609, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Broun, Pierre E.
; APPLICANT: Pineda, Onaira
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddies, James S.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.

; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: DuBell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kumimoto, Roderick
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; CURRENT FILING DATE: 2003-04-10
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142
; PRIOR FILING DATE: 2001-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1609
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Glycine max
US-10-412-699B-1609
Alignment Scores:
Pred. No.: 7,13e-27 Length: 974
Score: 247.00 Matches: 45
Percent Similarity: 90.74% Conservative: 4
Best Local Similarity: 83.33% Mismatches: 5
Query Match: 82.89% Indels: 0
DB: 18 Gaps: 0
US-10-666-642-194_COPY_111_164 (1-54) x US-10-412-699B-1609 (1-974)
Qy 1 AspGlyPheLysTrpArgLysTyTrGlyLysSerVallysAsnAenIleAsnLysArg 20
Db 582 GATGGATACAAAGTCGAGGAGTACGGCAAGAGTCCGCGAAGAGCAGTCCCAATCTAAGG 523
Qy 21 AsnTyTrtYrLysCysSerSxerGluGlyCysSerVallysLysArgValGluArgAspGly 40
Db 522 AACTACTACAAATGTTCAAGTGGAGGATGCGAGTGTGAAGAAAGGGTGGAAAGGGATAGA 463
Qy 41 AspAspAlaAlaTyTrValIleThrTyTrGluGlyValHis 54
Db 462 GATGACTACAGCTACGTCATCAACATATGATGAAGGTGTGCAC 421
RESULT 15
US-10-425-115-74300
; Sequence 74300, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B

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; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 74300
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_167760C.1
US-10-425-115-74300

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Alignment Scores:

Pred. No.:	1e-26	Length:	580
Score:	244.00	Matches:	43
Percent Similarity:	88.89%	Conservative:	5
Best Local Similarity:	79.63%	Mismatches:	6
Query Match:	81.88%	Indels:	0
DB:	20	Gaps:	0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-425-115-74300 (1-580)

Qy	1	AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnIleAsnLysArg	20
Db	389	GATGGATTCAATGGAGGAAGTATGCCAAGAAAGGCTGTCAAGAGTAGCCCAATCCAAGG	448
Qy	21	AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly	40
Db	449	AACTACTACCGCTGCTCGTGGAGGGCTGCGGCGTGAAGAACGGGTGGAGAGGCCGC	508
Qy	41	AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis	54
Db	509	GACGACCCCGCTACGTCAATCACCACCTACGACGGGCTCCAC	550

Search completed: August 26, 2005, 05:03:58
Job time : 527 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 25, 2005, 23:29:33 ; Search time 140 Seconds
(without alignments)

631.135 Million cell updates/sec

Title: US-10-666-642-194_COPY_111_164

Perfect score: 298

Sequence: 1 DGFWRKYGKSKVKNINKR.....RVERDGDAAAYVITTYEGVH 54

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO-epool/US10666642/runat 25082005 130054 24882/app query.fasta_1.199
-DB=Issued Patents NA -QFWT=fastcap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10666642@cgn 1.177 @runat 25082005 130054 24882 -NCPUS=6 -ICPU=3
-NO MAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	242	81.2	352	US-09-640-211A-1204	Sequence 1204, Ap
2	230	77.2	748	US-09-533-029-29	Sequence 29, Appl
3	197	66.1	724	US-09-533-029-15	Sequence 15, Appl
4	191	64.1	471	US-09-640-211A-1406	Sequence 1406, Ap
5	191	64.1	878	US-09-533-029-116	Sequence 116, App
6	190	63.8	527	US-09-640-211A-1849	Sequence 1849, Ap
7	187	62.8	378	US-09-640-211A-1841	Sequence 1841, Ap
8	165	55.4	306	US-09-313-294A-4059	Sequence 4059, Ap
9	158	53.0	162	US-09-640-211A-1219	Sequence 1219, Ap
10	157.5	52.9	296	US-09-640-211A-1509	Sequence 1509, Ap
11	154.5	51.8	1130	US-09-533-029-27	Sequence 27, Appl
12	153.5	51.5	561	US-09-640-211A-1580	Sequence 1580, Ap

13	151.5	50.8	1952	4	US-09-533-029-89	Sequence 89, Appl
14	145.5	48.8	319	4	US-09-640-211A-1487	Sequence 1487, Ap
15	145.5	48.8	1651	4	US-09-533-029-59	Sequence 59, Appl
16	145	48.7	385	4	US-09-640-211A-1531	Sequence 1531, Ap
17	137.5	46.1	351	4	US-09-640-211A-1694	Sequence 1694, Ap
18	137.5	46.1	468	4	US-09-640-211A-1504	Sequence 1504, Ap
19	130	43.6	337	4	US-09-640-211A-1309	Sequence 1309, Ap
20	129	43.3	340	4	US-09-640-211A-1498	Sequence 1498, Ap
21	127.5	42.8	1205	4	US-09-533-029-5	Sequence 5, Appl
22	123.5	41.4	360	4	US-09-640-211A-1358	Sequence 1358, Ap
23	120.5	40.4	557	4	US-09-640-211A-1435	Sequence 1435, Ap
24	117	39.3	520	4	US-09-640-211A-1238	Sequence 1238, Ap
25	116.5	39.1	1296	4	US-09-533-029-63	Sequence 63, Appl
26	112.5	37.8	425	4	US-09-640-211A-1434	Sequence 1434, Ap
27	104	34.9	567	4	US-09-640-211A-1269	Sequence 1269, Ap
28	103.5	34.7	1099	4	US-09-533-029-1	Sequence 1, Appl
29	88.5	29.7	2352	4	US-09-533-029-117	Sequence 117, Appl
30	75	25.2	351	4	US-09-640-211A-1248	Sequence 1248, Ap
31	65	21.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl
32	65	21.8	1664976	4	US-09-692-570-1	Sequence 16724, A
33	64	21.5	138693	4	US-09-949-016-16928	Sequence 16928, A
34	64	21.5	524032	4	US-09-949-016-16929	Sequence 16929, A
35	64	21.5	524032	4	US-09-949-016-16930	Sequence 16930, A
36	64	21.5	524032	4	US-09-949-016-16931	Sequence 16931, A
37	64	21.5	529885	4	US-09-949-016-14340	Sequence 14340, A
38	64	21.5	529885	4	US-09-949-016-14341	Sequence 14341, A
39	64	21.5	529885	4	US-09-949-016-14342	Sequence 14342, A
40	64	21.5	529885	4	US-09-949-016-14343	Sequence 14343, A
41	64	21.5	529885	4	US-09-949-016-14344	Sequence 14344, A
42	64	21.5	529885	4	US-09-949-016-14345	Sequence 14345, A
43	64	21.5	529885	4	US-09-949-016-14346	Sequence 14346, A
44	64	21.5	529885	4	US-09-949-016-14347	Sequence 14347, A
45	64	21.5	529885	4	US-09-949-016-14347	Sequence 14347, A

ALIGNMENTS

RESULT 1
US-09-640-211A-1204
; Sequence 1204, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1204
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1204

Alignment Scores: 6.51e-28 Length: 352
Pred. No.: 242.00 Matches: 43
Score: 242.00
Percent Similarity: 85.19% Conservative: 3
Best Local Similarity: 79.63% Mismatches: 8
Query Match: 81.21% Indels: 0
DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1204 (1-352)

Qy 1 AspGlyPheLysTrpArgLysTrpGlyLysSerVallysAsnAsnLysArg 20
Db 184 GACGGATTCAAGTGGAGGAGTACCGGAGAGAGATGCTGTGAGACAGTCCGATCCGAGG 243

QY 21 AsnTyrTyLysCysSerSerGluGlyCysSerValLysLysValGluArgAspGly 40
 |||||:::|||||
 Db 244 AACTACTCGGTGTCGTGGAGGCTGCTGTGGAAGAGAGTGCACGGGACAGA 303
 |||||:::|||||
 QY 41 AspAspAlaAlaTyrValLleThrThrTyrGluGlyValHis 54
 |||||:::|||||
 Db 304 GACGACCAAGGTATGTAATAACAACATACGAGGGCATCCAT 345
 |||||:::|||||

RESULT 2

US-09-533-029-29

; Sequence 29, Application US/09533029

; Patent No. 6664446

; GENERAL INFORMATION:

; APPLICANT: Heard, Jacqueline

; APPLICANT: Broun, Pierre

; APPLICANT: Riechmann, Jose-Luis

; APPLICANT: Keddle, James

; APPLICANT: Pineda, Omaira

; APPLICANT: Adam, Luc

; APPLICANT: Samaha, Raymond

; APPLICANT: Zhang, James

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Ratcliffe, Oliver

; APPLICANT: Pilgrim, Marsha

; APPLICANT: Jiang, Cai-Zhong

; APPLICANT: Reuber, Lynne

; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES

; FILE REFERENCE: MBI-010

; CURRENT APPLICATION NUMBER: US/09/533,029

; CURRENT FILING DATE: 2000-03-22

; EARLIER APPLICATION NUMBER: 60/125,814

; EARLIER FILING DATE: 1999-03-23

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 29

; LENGTH: 748

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; OTHER INFORMATION: G1275

; US-09-533-029-29

Alignment Scores:

Pred. No.: 1,28e-25 Length: 748
 Score: 230.00 Matches: 41
 Percent Similarity: 85.19% Conservative: 5
 Best Local Similarity: 75.93% Mismatches: 8
 Query Match: 77.18% Indels: 0
 DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-29 (1-748)

QY 1 AspGlyPheLysTyrArgLysTyrGlyLysLysSerValLysAsnAsnLleAsnLysArg 20
 |||||:::|||||
 Db 397 GACGGGTTCAAGTGGAGAAAGTATGGAGAGAGATGTTGGAAGACAGCCCATCCAAGA 456
 |||||:::|||||

QY 21 AsnTyrTyLysCysSerSerGluGlyCysSerValLysLysValGluArgAspGly 40
 |||||:::|||||
 Db 457 AACTACTACAAATGTTCAAGTTCGCTGCCCGGAGAGAAAGGGTTGAACGACAGAGA 516
 |||||:::|||||

QY 41 AspAspAlaAlaTyrValLleThrThrTyrGluGlyValHis 54

|||||:::|||||

Db 517 GATGATCCGAGCTTGTGATACACTTACGAGGGTTCCAC 558

|||||:::|||||

RESULT 3

US-09-533-029-15

; Sequence 15, Application US/09533029

; Patent No. 6664446

; GENERAL INFORMATION:

; APPLICANT: Heard, Jacqueline

; APPLICANT: Broun, Pierre

; APPLICANT: Riechmann, Jose-Luis

; APPLICANT: Keddle, James

; APPLICANT: Pineda, Omaira
 ; APPLICANT: Adam, Luc
 ; APPLICANT: Samaha, Raymond
 ; APPLICANT: Zhang, James
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Ratcliffe, Oliver
 ; APPLICANT: Pilgrim, Marsha
 ; APPLICANT: Jiang, Cai-Zhong
 ; APPLICANT: Reuber, Lynne
 ; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES

; FILE REFERENCE: MBI-010

; CURRENT APPLICATION NUMBER: US/09/533,029

; CURRENT FILING DATE: 2000-03-22

; EARLIER APPLICATION NUMBER: 60/125,814

; EARLIER FILING DATE: 1999-03-23

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 15

; LENGTH: 724

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; OTHER INFORMATION: G179

; US-09-533-029-15

Alignment Scores:

Pred. No.: 1,34e-20 Length: 724
 Score: 197.00 Matches: 33
 Percent Similarity: 79.63% Conservative: 10
 Best Local Similarity: 61.11% Mismatches: 11
 Query Match: 66.11% Indels: 0
 DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-15 (1-724)

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 |||||:::|||||
 Db 263 GATGGATACAGTGGAGAGTACGGCCAAAAGCAGTCAAGAACAAATCCATTCCCCAGG 322
 |||||:::|||||

QY 21 AsnTyrTyLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
 ::|||:::|||||
 Db 323 AGCTATTATTAAGTCACAGAGAAGGATGCGAGGTGAAGACGACGAGTGCAGAGGCAATGG 382
 |||||:::|||||

QY 41 AspAspAlaAlaTyrValLleThrThrTyrGluGlyValHis 54

|||||:::|||||

Db 383 GGACAGCAGAGGTGGTGGTGCACCATACCAAGGTGTTCTAT 424

|||||:::|||||

RESULT 4

US-09-640-211A-1406

; Sequence 1406, Application US/09640211A

; Patent No. 6833446

; GENERAL INFORMATION:

; APPLICANT: Wood, Marion

; APPLICANT: Shenk, Michael A.

; APPLICANT: McGrath, Annette

; APPLICANT: Glenn, Matthew

; TITLE OF INVENTION: Compositions and Methods for the

; FILE OF INVENTION: Modification of Gene Transcription

; FILE REFERENCE: 11000.1021C1U

; CURRENT APPLICATION NUMBER: US/09/640,211A

; CURRENT FILING DATE: 2000-08-16

; NUMBER OF SEQ ID NOS: 2368

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1406

; LENGTH: 471

; TYPE: DNA

; ORGANISM: Eucalyptus grandis

; US-09-640-211A-1406

Alignment Scores:

Pred. No.: 6,05e-20 Length: 471
 Score: 191.00 Matches: 33
 Percent Similarity: 77.78% Conservative: 9

US-09-533-029-27
; Sequence 27, Application US/09533029
; Patent No. 6664446

GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre

APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddle, James
; APPLICANT: Pineda, Omaira

APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James

APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha

APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES

FILE REFERENCE: MEI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22

EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1130

TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:

OTHER INFORMATION: G291
; FEATURE:
; OTHER INFORMATION: "n" bases at various positions throughout the

OTHER INFORMATION: sequence may be A, T, C, G, other or unknown
US-09-533-029-27

Alignment Scores:
Pred. No.: 7,77e-14 Length: 1130

Score: 154.50 Matches: 26
Percent Similarity: 74.55% Conservative: 15

Best Local Similarity: 47.27% Mismatches: 13
Query Match: 51.85% Indels: 1

DB: 4 Gaps: 1

US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-27 (1-1130)

Qy 1 AspGlyPheLysTpaTqLysTyrGlyLysSerVallysAenAenLysArg 20

Db 554 GATGGGTATCAATGAGGAAATATGGACAGAAAGTGACTAGAGACAATCCATCTCCCAAGA 613

Qy 21 AsnTyrTyLysCysSer---SerGluGlyCysSerVallysArgValGluArgAsp 39

Db 614 GCTTACTTCAATGTGCTGCTCCAGCTGTTCTGTCAAAAGAGAGTTTCAGAGAGT 673

Qy 40 GlyAspAlaAlaTyrValIleThrTyrGluGlyValHis 54

Db 674 GTGAGGATCATGCTCGTGTAGTTCACATTTATGAGGGTGAACAC 718

RESULT 12

US-09-640-211A-1580

; Sequence 1580, Application US/09640211A

; Patent No. 6833446

GENERAL INFORMATION:
; APPLICANT: Wood, Marion

APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette

APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the

FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A

NUMBER OF SEQ ID NOS: 2368

Alignment Scores:
Pred. No.: 4.8e-13 Length: 1952

Score: 151.50 Matches: 28
Percent Similarity: 70.91% Conservative: 11

Best Local Similarity: 50.91% Mismatches: 15
Query Match: 50.84% Indels: 1

DB: 4 Gaps: 1

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1580 (1-561)

Qy 1 AspGlyPheLysTpaTqLysTyrGlyLysSerVallysAenAenLysArg 20

Db 272 GATGAATTCATGGCGGAAATATGGACAGCCCAATTAAGGGCTCTCCACATCCCAAGA 331

Qy 21 AsnTyrTyLysCysSer---GluGlyCysSerVallysArgValGluArgAsp 39

Db 332 GGTATTACAAATGCACACATGAGAGGTTCCTCACAAGAAAGCAGTAGAACGGGCC 391

Qy 40 GlyAspAlaAlaTyrValIleThrTyrGluGlyValHis 54

Db 392 CTGACGATCCAAACGATTGATTGTAACATATGAGGGCGAACAC 436

RESULT 13

US-09-533-029-89

; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 1580
; LENGTH: 561

TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-1580

Alignment Scores:
Pred. No.: 4.14e-14 Length: 561

Score: 153.50 Matches: 29
Percent Similarity: 65.45% Conservative: 7

Best Local Similarity: 52.73% Mismatches: 18
Query Match: 51.51% Indels: 1

DB: 4 Gaps: 1

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1580 (1-561)

Qy 1 AspGlyPheLysTpaTqLysTyrGlyLysSerVallysAenAenLysArg 20

Db 272 GATGAATTCATGGCGGAAATATGGACAGCCCAATTAAGGGCTCTCCACATCCCAAGA 331

Qy 21 AsnTyrTyLysCysSer---GluGlyCysSerVallysArgValGluArgAsp 39

Db 332 GGTATTACAAATGCACACATGAGAGGTTCCTCACAAGAAAGCAGTAGAACGGGCC 391

Qy 40 GlyAspAlaAlaTyrValIleThrTyrGluGlyValHis 54

Db 392 CTGACGATCCAAACGATTGATTGTAACATATGAGGGCGAACAC 436

RESULT 13

US-09-533-029-89

; Sequence 89, Application US/09533029

; Patent No. 6664446

GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline

APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis

APPLICANT: Keddle, James
; APPLICANT: Pineda, Omaira

APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond

APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang

APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha

APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne

TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MEI-010

CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22

EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23

NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 89
; LENGTH: 1952

TYPE: DNA
; ORGANISM: Arabidopsis thaliana

FEATURE:
; OTHER INFORMATION: G186

FEATURE:
; OTHER INFORMATION: "n" bases at various positions throughout the

OTHER INFORMATION: sequence may be A, T, C, G, other or unknown
US-09-533-029-89

Alignment Scores:
Pred. No.: 4.8e-13 Length: 1952

Score: 151.50 Matches: 28
Percent Similarity: 70.91% Conservative: 11

Best Local Similarity: 50.91% Mismatches: 15
Query Match: 50.84% Indels: 1

DB: 4 Gaps: 1

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US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-89 (1-1952)
QY 1 AspGlyPheLysTyrArgLysTyrGlyLysLysSerValLysAsnAsnIleAsnLysArg 20
DB 1036 GATGGATGTCAATGGAGAAATATGCCAGAGATGGCCAAAGGAATCCTTGTCCGCGG 1095
QY 21 AsnTyrTyrLysCysSer---SerGluGlyCysSerValLysLysArgValGluArgAsp 39
DB 1096 GCATATTACCGCTGCACGATGGCCACGGGCTGCCGTTGCCAAACAAGTTCAAGTTGC 1155
QY 40 GlyAspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
DB 1156 GCGGAAGACAGATCAATCTGTATTACACCTACGAGGGAACCAT 1200

RESULT 14
US-09-640-211A-1487
; Sequence 1487, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1487
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1487
Alignment Scores:
Pred. No.: 3,12e-13 Length: 319
Score: 145.50 Matches: 25
Percent Similarity: 69.0% Conservative: 13
Best Local Similarity: 45.45% Mismatches: 16
Query Match: 48.83% Indels: 1
DB: 4 Gaps: 1
US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1487 (1-319)
QY 1 AspGlyPheLysTyrArgLysTyrGlyLysLysSerValLysAsnAsnIleAsnLysArg 20
DB 146 GATGGACACCACTGGAGGAAGTATGGCAAAAGATCACCAGGGACACCCCTTGTCCACGA 205
QY 21 AsnTyrTyrLysCysSer---SerGluGlyCysSerValLysLysArgValGluArgAsp 39
DB 206 GCTTACTCAATGGCTCCAGCTCCAGCTCCCTTGTCAAGAGAGGTGCAAGAAGT 265
QY 40 GlyAspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
DB 266 GCTGAAGACCATCGTCACTATGCGACTTATGAAGGCGACAC 310

RESULT 15
US-09-533-029-59
; Sequence 59, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
```

```
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1993-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 59
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1417
US-09-533-029-59
Alignment Scores:
Pred. No.: 3,13e-12 Length: 1651
Score: 145.50 Matches: 27
Percent Similarity: 67.27% Conservative: 10
Best Local Similarity: 49.09% Mismatches: 17
Query Match: 48.83% Indels: 1
DB: 4 Gaps: 1
US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-59 (1-1651)
QY 1 AspGlyPheLysTyrArgLysTyrGlyLysLysSerValLysAsnAsnIleAsnLysArg 20
DB 749 GACGGATGTCAATGGAGAAATATCGGTCAAGAAATGGCGAAAGGAATCCATGTCTCTGC 808
QY 21 AsnTyrTyrLysCysSer---SerGluGlyCysSerValLysLysArgValGluArgAsp 39
DB 809 GCTTATTATCGTTGCACCAATGCGGTGGATGTCCTGTCCTAACACAGGTCCACAGATGC 868
QY 40 GlyAspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
DB 869 GCGGAGGATACAATCTATCTTGACACACACGATACGAGGAAACCAT 913

Search completed: August 26, 2005, 01:48:30
Job time : 149 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 25, 2005, 19:45:28 ; Search time 2856 Seconds
(without alignments)
916.170 Million cell updates/sec

Title: US-10-666-642-194_COPY_111_164

Perfect score: 298

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

.Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ats.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	242	81.2	839	8	AY341854 Oryza sat

c	5	242	81.2	149699	8	AP002486	Oryza sat
	6	237	79.5	1193	8	AK108555	Oryza sat
	7	232	77.9	983	8	AY341846	Oryza sat
	8	232	77.9	1091	8	AK108522	Oryza sat
	9	230	77.2	522	8	AY071847	Arabidops
	10	230	77.2	748	6	AR439815	Sequence
	11	197	66.1	444	8	AF426251	Arabidops
	12	197	66.1	548	8	AY085246	Arabidops
	13	197	66.1	696	8	AK118457	Arabidops
	14	197	66.1	724	6	AR439808	Sequence
	15	197	66.1	1200	8	AF442397	Arabidops
	16	197	66.1	1231	8	AY091224	Arabidops
	17	197	66.1	1809	8	AY083870	Arabidops
	18	196	65.8	147704	8	AC097112	Oryza sat
	19	195	65.4	1182	6	AX506986	Sequence
	20	195	65.4	1182	6	AX652016	Sequence
	21	195	65.4	1182	6	BT008482	Arabidops
	22	195	65.4	1182	8	AF418309	Arabidops
	23	195	65.4	1213	8	BT002338	Arabidops
	24	195	65.4	1264	8	AY114650	Arabidops
	25	195	65.4	1453	8	AY062720	Arabidops
	26	195	65.4	1462	8	AY045813	Arabidops
	27	195	65.4	1606	8	AY136318	Arabidops
	28	195	65.4	1667	8	CUSLDB	Sequence
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	32	194	65.1	1046	8	AK069091	Oryza sat
	33	194	65.1	1070	8	AY341858	Oryza sat
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	36	193	64.8	1847	8	AF459793	Oryza sat
	37	193	64.8	1993	8	IPBSPFLP	Sequence
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	39	193	64.8	2764	8	AK065078	Oryza sat
	40	192	64.4	1287	8	AK062027	Oryza sat
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	42	192	64.4	2353	8	AK065518	Oryza sat
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	45	191	64.1	657	8	AF404857	Arabidops

ALIGNMENTS

RESULT 1	AF426252	Arabidopsis thaliana WRKY transcription factor 51 (WRKY51) mRNA, complete cds.	585 bp	mRNA	linear	PLN 08-NOV-2001
LOCUS	AF426252	Arabidopsis thaliana (thale cress)				
DEFINITION	AF426252	Arabidopsis thaliana (thale cress)				
ACCESSION	AF426252	GI:16798361				
VERSION	AF426252.1					
KEYWORDS						
SOURCE		Arabidopsis thaliana (thale cress)				
ORGANISM		Arabidopsis thaliana				
REFERENCE		Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.				
AUTHORS		1 (bases 1 to 585)				
TITLE		Kushnir, S., Ulker, B. and Somssich, I.E.				
JOURNAL		Submitted (02-OCT-2001) Biochemistry, Max-Planck-Institut fur Zuchtungsforchung, Carl-von-Linne-Weg 10, Koeln, NRW D-50829, Germany				
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		/tissue_type="inflorescence"				
		/ecotype="Columbia"				

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          /db_xref="GI:16798362"
          /translation="WNISQNPSTFYSDENFINPFWNDNDFSNLMPFFIDEGNGN
LIEEISPTSVISSETFTGSGSGSATTLISKESTNRGSKESQTKETGHRVAFRI
RSKIDVMDGDFKRWIKYKGRKVNKNINKNYKCSGSEGVKRRVERDGDAAAYVITTY
EGVHNHESLSNYYNEWVLSYDHDNQHSLRS"
ORIGIN
Alignment Scores:
Pred. No.: 1,07e-30 Length: 585
Score: 298.00 Matches: 54
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x AF426252 (1-585)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAsnLysArg 20
Db 331 GATGGTTTAAATGCGAGGAAGTATGCGAAGAATCTGTCAAAAACACATTACAGAGG 390

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgSpGly 40
Db 391 AATTACTACAAATGCTCAAGTGAAGGTTCTCGTGAAGAGAGGGGTAGAGAGATGGT 450

QY 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
Db 451 GACGATCGACGCTTATGTAAATTACACATATGAAGGAGTCCAT 492

RESULT 2
LOCUS AK109578 707 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:002-135-F06, full
insert sequence.
ACCESSION AK109578
VERSION AK109578.1 GI:32994787
KEYWORDS FLI CDNA; oligo capping.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team;
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Ootomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashizume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saitoh,H., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Tagaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasuunishi,A. and Hayashizaki,Y.
TITLE Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
JOURNAL Science 301 (5631), 376-379 (2003)
MEDLINE 22752273
PUBMED 12869764
REFERENCE 2 (bases 1 to 707)

```

AUTHORS

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kagawa,S., Kato,H., Kawagashira,N., Kawai,J., Kawamata,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Namiiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K.,
Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H.,
Osato,N., Ota,Y., Ootomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasuunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.

Direct Submission

TITLE

JOURNAL

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)

COMMENT

This clone is one of the 28K full-length cDNA clones from japonica
rice.

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.

FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasuunishi,A. and Hayashizaki,Y.

FEATURES

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Best Local Similarity: 75.93% Mismatches: 6
Query Match: 81.21% Indels: 0
DB: 8 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x AK109578 (1-707)

Qy 1 AspGlyPheLysTrpArgLysTrpGlyLysSerVallysAenAenilleAenLysArg 20
 Db 245 GACGGTTCAGAGTGCAGAAAGTACGGGAAGAGCGGTGAAGAGCAGCGCCGCGG 304
 Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerVallysLysArgValGluArgAspGly 40
 Db 305 AACTACTACCGGTGCTCGCGCGCGGGGTCGGCGTCAAGAGCGGTGAGCGGACGCGC 364
 Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
 Db 365 GACGACCGCGCTACGTGTCACCACTACGACGCGGTCCAC 406

RESULT 3
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 LOCUS
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 AK066252 792 bp mRNA linear PLN 24-JUL-2003
 AK066252.1 GI:32976270
 FLY CDNA; CAP trapper.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
 1
 The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Maeda, H., Kobayashi, M., Xie, Q., Lu, M., Nariwaka, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Oka, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

TITLE Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 JOURNAL Science 301 (5631), 376-379 (2003)
 MEDLINE 22752273
 PUBMED 12869764

REFERENCE
 2 (bases 1 to 792)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Maeda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariwaka, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

TITLE Direct Submission
 JOURNAL Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of

Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
 Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.

COMMENT

URL : http://cdna01.dna.affrc.go.jp/cdna/
 NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.
 FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariwaka, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Oca, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

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 Best Local Similarity: 77.78% Mismatches: 5
 Query Match: 81.21% Indels: 0
 DB: 8 Gaps: 0

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Qy 1 AspGlyPheLysTrpArgLysTrpGlyLysSerVallysAenAenilleAenLysArg 20
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 Db 404 AACTACTACCGGTGCTCGACGCGGGGTGCAACGCTGAAGAGCGGTGAGAGACCGG 463
 Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
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 ACCESSION AY341854
 VERSION AY341854.1 GI:33519195
 KEYWORDS
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 839)
Yao,Q., Peng,R. and Xiong,A.
Isolation of rice WRKY protein through W-box bait vector by
modified yeast one-hybrid system method
Unpublished
2 (bases 1 to 839)
Yao,Q., Peng,R. and Xiong,A.
Direct Submission
Submitted (14-JUL-2003) Bio-tech Center, Shanghai Academy of
Agricultural Science, Beidi Road 2901, Shanghai, Shanghai
021-201106, China
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Alignment Scores:
Pred. No.: 5,73e-23 Length: 839
Score: 242.00 Matches: 41
Percent Similarity: 88.89% Conservative: 7
Best Local Similarity: 75.93% Mismatches: 6
Query Match: 81.21% Indels: 0
DB: 8 Gaps: 0
US-10-666-642-194_COPY_111_164 (1-54) x AY341854 (1-839)
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QY 21 AnTYrTYrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgSpGly 40
Db 448 AACTACTACCGGTCTCGCGCGGGGTGCGGCGTCAAGAGCGGTGAGCGCGACGCG 507
QY 41 AspAspAlaAlaTyrValIleThrThrTYrTYrGluGlyValHis 54
Db 508 GACGACCCCGCTACGTCTGTCACCACTACGAGCGGTCCAC 549
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LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
PAC clone: P0510F03.
ACCESSION
AP002486 BA000010
VERSION
AP002486.1 GI:8468048
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1
Sasaki,T., Matsuoto,T., Yamamoto,K., Sakata,K., Baba,T.,
Katayose,Y., Wu,J., Nimura,Y., Cheng,Z., Nagamura,Y.,
Antonio,B.A., Kanamori,H., Hosokawa,S., Masukawa,M., Arikawa,K.,
Chiden,Y., Hayashi,M., Okamoto,M., Ando,T., Aoki,H., Arita,K.,
Hamada,M., Harada,C., Hijishita,S., Honda,M., Ichikawa,Y.,
Idonuma,A., Iijima,M., Ikeda,M., Ikono,M., Ito,S., Ito,T., Ito,Y.,
Ito,Y., Iwabuchi,A., Kamiya,K., Karasawa,W., Katagiri,S.,
Kikuta,A., Kobayashi,N., Kono,I., Machita,K., Maehara,T.,
Mizuno,H., Mizubayashi,T., Mukai,Y., Negaseki,H., Nakashima,M.,
Nakama,Y., Nakamichi,Y., Nakamura,M., Namiki,N., Negishi,M.,
Ohta,I., Ono,N., Saji,S., Sakai,K., Shibata,M., Shimokawa,T.,
Shomura,A., Song,J., Takazaki,Y., Terasawa,K., Tsuji,K., Waki,K.,
Yamagata,H., Yamane,H., Yoshiki,S., Yoshihara,R., Yukawa,K.,
Zhong,H., Iwama,H., Endo,T., Ito,H., Hahn,J.H., Kim,H.I., Eun,M.Y.,
Yano,M., Jiang,J. and Gojobori,T.
The genome sequence and structure of rice chromosome 1
Nature 420 (6913), 312-316 (2002)
22337376
PUBMED
12447438
2 (bases 1 to 149699)
Sasaki,T., Matsuoto,T. and Yamamoto,K.
Direct Submission
Submitted (07-JUN-2000) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
The orientation of the sequence is from SP6 to T7 of the PAC clone.
Genes were predicted from the integrated results of the
following:GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as
SplicePredictor (October1998 version). The genomic sequence was
searched against the non-redundant database NRP (PIR,SWISSPROT,
GENPEPT, PDB) from MAFY DNABank and the cDNA sequence database at
RGP. Protein similarities of the coding regions were searched
against NRP with BLASTP2.0. ESTs represent the identified cDNA
sequences using BLASTN2.0 with the corresponding DDBJ accession no.
and RGP clone ID.
This sequence of this clone has an overlap with P0695A04 clone at
the 3' end. This clone ends at the position 22,228 of P0695A04.
Detailed information on overlap and assembly quality together with
annotation of this entry at
http://rgp.dna.affrc.go.jp/GenomeSeq.html.
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AUTHORS

The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team:
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yarak, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nishihiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., Riken: Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 Science 301 (5631), 376-379 (2003)
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2 (bases 1 to 1193)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, J., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, K., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuka, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyota, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

Direct Submission

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan [E-mail: skikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007]

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yarak, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., and Yamamoto, M.
 FALS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,

FEATURES

source
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ORIGIN

Alignment Scores: 4.06e-22 Length: 1193
 Pred. No.: 237.00 Matches: 40
 Score: 88.89% Conservative: 8
 Percent Similarity: 74.07% Mismatches: 6
 Best Local Similarity: 79.53% Indels: 0
 Query Match: 8 Gaps: 0
 DB:

US-10-666-642-194_COPY_111_164 (1-54) x AK108555 (1-1193)

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Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerVallysLysArgValGluArgAspGly 40

Db 575 AACTACTACCGGTGCTCGACGGGGGTGCAACGTGAAGAGAGGGTGGAGAGACAAAG 634

Qy 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54

Db 635 AACGACCGCGGTACGTGCGTACGATGACGGGGATCCAC 676

RESULT 7

AY341846

LOCUS

AY341846

DEFINITION

AY341846

ACCESSION

AY341846.1

VERSION

GI:33519179

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 983)

Yao, Q., Peng, R. and Xiong, A.

Isolation of rice WRKY protein through W-box bait vector by modified yeast one-hybrid system method

Unpublished

2 (bases 1 to 983)

Yao, Q., Peng, R. and Xiong, A.

Direct Submission

Submitted (14-JUL-2003) Bio-Tech Center, Shanghai Academy of Agricultural Science, Beidi Road 2901, Shanghai, Shanghai 021-201106, China

Location/Qualifiers

1. 983

/organism="Oryza sativa (japonica cultivar-group)"

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/db_xref="taxon:39947"

40..780

/note="transcription factor"

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CDS

RCSGCGRVKVRERDDARFVVTVDGVNHPAPLHLRQPLPPPGGYSIAGAPAVV
APHGRGLGEEAEVIALFRGTTATSLILP*

ORIGIN

Alignment Scores:
Pred. No.: 1,53e-21 Length: 983
Score: 232.00 Matches: 40
Percent Similarity: 87.04% Conservative: 7
Best Local Similarity: 74.07% Mismatches: 7
Query Match: 77.85% Indels: 0
DB: 8 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x AY341846 (1-983)

Qy 1 AspGlyPheLysTrpArgLysTyTcGlyLysLysSerValLysAsnAenLysArg 20
Db 451 GACGGCTACCGGTGGAGGAAGTACGGCAAGAAGATGGTCAAGAACAGCCCCAACCCCAAGG 510
Qy 21 AsnTyTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
Db 511 AACTACTACCGGTGCTCGAGCGAGGGGTGCGCGGTGAAGAGCGGTGGAGCGCGCCGG 570
Qy 41 AspAlaAlaLysValLysThrThrTyrGluGlyValHis 54
Db 571 GACGACGGCGCTCGTCTGCTCACCACCTACGACGCGCTCCAC 612

RESULT 8

AK108522
LOCUS AK108522 1091 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:002-144-B05, full insert sequence.

ACCESSION

AK108522.1 GI:32993731

KEYWORDS

FLI cDNA; oligo capping

SOURCE

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team,
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Otono, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Ootani, K., Oka, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)

TITLE

japonica rice

JOURNAL

Science 301 (5631), 376-379 (2003)

MEDLINE

22752273

REFERENCE

2 (bases 1 to 1091)

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiroaka, T.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,

Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
Namiki, T., Narikawa, R., Niikura, J., Nishii, K., Nomura, K.,
Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
Osato, N., Ota, Y., Otono, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and
Yoshimura, A.

Direct Submission

TITLE

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp).

Tel: 81-29-838-7007, Fax: 81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica
rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and
Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Otono, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ooka, H., Ooka, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kouda, M.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Oka, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
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Sogabe, Y., Sugami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A., and Hayashizaki, Y.

FEATURES

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ORIGIN

Alignment Scores:
Pred. No.: 1,73e-21 Length: 1091
Score: 232.00 Matches: 40
Percent Similarity: 87.04% Conservative: 7
Best Local Similarity: 74.07% Mismatches: 7
Query Match: 77.85% Indels: 0
DB: 8 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x AK108522 (1-1091)

Qy 1 AspGlyPheLysTrpArgLysTyTcGlyLysLysSerValLysAsnAenLysArg 20

Db 455 GACGGCTACCGGTGGAGGAAGTACGGCAAGAAGATGGTCAAGAACAGCCCCAACCCCAAGG 514

Qy 21 AsnTyTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40

Db 515 AACTACTACCGGTGCTCGAGCGAGGGGTGCGCGGTGAAGAGCGGTGGAGCGCGCCGG 574

Qy 41 AspAlaAlaLysValLysThrThrTyrGluGlyValHis 54

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Db 575 GACGAGCGCGCTCGTGTCTACCACTAGCAGCGGTCCAC 616
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RESULT 9
AY071847
LOCUS
DEFINITION Arabidopsis thaliana WRKY transcription factor 50 (WRKY50) mRNA,
complete cds.
ACCESSION AY071847
VERSION AY071847.1 GI:18252116
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 522)
AUTHORS Ulker,B., Kuhnir,S. and Somssich,I.E.
TITLE Arabidopsis thaliana transcription factor WRKY50
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 522)
AUTHORS Ulker,B., Kuhnir,S. and Somssich,I.E.
TITLE Direct Submission
JOURNAL Submitted (26-DEC-2001) Biochemistry, Max-Planck-Institut fur
Zuchtungsforchung, Carl-von-Linne-Weg 10, Koeln, NRW D-50829,
Germany
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 1,37e-21 Length: 522
Score: 230.00 Matches: 41
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Best Local Similarity: 75.93% Mismatches: 8
Query Match: 77.18% Indels: 0
DB: 8 Gaps: 0
US-10-666-642-194_COPY_111_164 (1-54) x AY071847 (1-522)
Qy 1 AspGlyPheLysTyrArgLysTyrGlyLysLysSerValLysAsnAsnLysArg 20
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Db 340 GACGGGTTCAAGTGAGAAAGTATGGGAAGAAGATGGTGAAGAACAGCCCATCAAGA 399
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Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
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Db 400 AACTACTACAAATGTTTCAGTTGATGCTGCTCCGCTGAAGAAAAGGTTGAACGACGACAGA 459
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Qy 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
|||||:::|||||:::|||||:::|||||:::|||||
Db 460 GATGATCCGAGCTTTGTGATACACTTACGAGGGTTCCAC 501
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RESULT 10
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LOCUS
DEFINITION Arabidopsis thaliana WRKY transcription factor 45 (WRKY45) mRNA,
complete cds.
ACCESSION AR439815
VERSION AR439815.1 GI:16798359
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 444)
AUTHORS Kuhnir,S., Ulker,B. and Somssich,I.E.
TITLE Direct Submission
JOURNAL Submitted (02-OCT-2001) Biochemistry, Max-Planck-Institut fur
Zuchtungsforchung, Carl-von-Linne-Weg 10, Koeln, NRW D-50829,
Germany
FEATURES
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TNEENKK"

ORIGIN

Alignment Scores:
Pred. No.: 1.01e-16 Length: 1200
Score: 197.00 Matches: 33
Percent Similarity: 81.48% Conservative: 11
Best Local Similarity: 61.11% Mismatches: 10
Query Match: 66.11% Indels: 0
DB: 8 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x AF442397 (1-1200)

Qy	1	AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnLysArg	20
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Db	724	AGCTATTACCGTTGCACCCACAGTGGGTTGCGAGTGAAGAGAGAGTGGAGATCCTCC	783
Qy	41	AspAspAlaAlaTyrValIleThrTyrGluGlyValHis	54
Db	784	GATGATCCTTCGATCGTCATGACCAACCTACGAGGTCAGCAT	825

Search completed: August 26, 2005, 01:06:40
Job time : 2881 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 25, 2005, 23:22:33 ; Search time 2304 Seconds
(without alignments)
892.131 Million cell updates/sec

Title: US-10-666-642-194_COPY_111_164

Perfect score: 298

Sequence: 1 DGFWRKYGKSKVRNNINR.....RVERGDGDAAYVITYEGVH 54

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPTO_epool/US10666642/runat_25082005_130054_24868/app_query.fasta_1.199
-DB=EST -QFMT=fa5cap -SUFFIX=rst -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
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6: gb_est5:*
7: gb_est6:*
8: gb_g881:*
9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	298	100.0	435	6	CD529340
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5	250	83.9	549	2	BF009428
6	250	83.9	634	5	BU547499
7	250	83.9	671	4	BI209002
8	249	83.6	412	5	BQ515840
9	249	83.6	418	4	BI433746

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15	249	83.6	610	4	BM328984
16	249	83.6	690	2	AW565483
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30	245	82.2	573	6	CB879922
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32	244	81.9	673	5	BQ987474
33	244	81.9	710	5	BQ984602
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35	243	81.5	649	6	CD233113
36	242	81.2	585	9	CL970459
37	242	81.2	601	2	BE230596
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39	240	80.5	727	7	CO817603
40	239	80.2	559	5	BU577163
41	239	80.2	596	5	BQ742659
42	239	80.2	744	7	CO093096
c 43	239	80.2	745	7	CO093095
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45	239	80.2	819	7	CN140156

RESULT 1
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LOCUS
DEFINITION 02J01 Arabidopsis leaf Senescence Library Arabidopsis thaliana CDNA 3', mRNA sequence.
ACCESSION CD529340
VERSION CD529340.1 GI:40449352
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 435)
AUTHORS Guo,Y., Cai,Z. and Gan,S.
TITLE Transcriptome of Arabidopsis leaf senescence
JOURNAL Plant Cell Environ. 27 (5), 521-549 (2004)
COMMENT Contact: Susheng Gan
Department of Horticulture
Cornell University
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
Tel: 607 254 5418
Fax: 607 255 0599
Email: sg288@cornell.edu
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CD529340
CD529340.1 GI:40449352
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 435)
Guo,Y., Cai,Z. and Gan,S.
Transcriptome of Arabidopsis leaf senescence
Plant Cell Environ. 27 (5), 521-549 (2004)
Contact: Susheng Gan
Department of Horticulture
Cornell University
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
Tel: 607 254 5418
Fax: 607 255 0599
Email: sg288@cornell.edu
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and #6 (counted from the bottom) were harvested and
immediately frozen in liquid N2. The leaves were visibly
yellow excepted for the leaf base areas that were still
greenish."

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ORIGIN

```

Alignment Scores:
Pred. No.: 1,13e-31 Length: 435
Score: 288.00 Matches: 54
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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US-10-666-642-194_COPY_111_164 (1-54) x CD529340 (1-435)

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QY 1 AspGlyPheLysTrpArgLysTyrgLyLysSerValLysAsnAsnLeAsnLysArg 20
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DB 215 GATGGTTTAAATGGAGGAAGTATGGCAAGAAATCTGTCAAAAACAACATTAAACAAGAGG 274
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QY 21 AantTyrrLysCyseSerSerGluGlyCyseSerValLysLysArgValGluArgAspGly 40
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DB 275 AATTACTACAATGCTCAAGTGAAGTCTCGGTGAAGAGGAGGTAGAGAGATGCT 334
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QY 41 AspAspAlaAlaTyrrValIleThrThrTyrrGluGlyValHis 54
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DB 335 GACGATGCAGCTTATGTAATTACACATATGAGAGTCCAT 376
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RESULT 2

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CB879380
LOCUS CB879380 643 bp mRNA linear EST 23-APR-2003
DEFINITION HP11P20T HP Hordeum vulgare subsp. vulgare cDNA clone HP11P20
5-PRIME mRNA sequence.

```

```

ACCESSION CB879380
VERSION CB879380.1 GI:30081366
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.

```

```

REFERENCE
1 (bases 1 to 643)
Zhang,H., Weschke,W., Michalek,W., Stein,N. and Graner,A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils

```

```

AUTHORS Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Correnstr. 3, 06466, Gatersleben, Germany

```

```

TITLE Tel: 039482-5522
JOURNAL Tel: 039482-5522
COMMENT Fax: 039482-5595

```

```

Email: stein@ipk-gatersleben.de
Insert Length: 643 Std Error: 0.00
Plate: 11 row: P column: 20
Seq primer: T3.

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Location/Qualifiers
1..643
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:538869"
/db_xref="taxon:112509"
/clone="HP11P20"
/tissue_type="epidermis"
/dev_stage="seedlings grown in greenhouse for 6 days"
/lab_host="Xl10-Gold"

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FEATURES

source

```

1..700
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HW01B17T"
/tissue_type="roots"
/lab_host="XL0LR"
/clone_lib="Hordeum vulgare Barke roots"
/note="Vector: plasmid pBK-CMV; Site 1: EcoRI; Site 2:
XhoI; mRNA was made from roots of spring barley variety
'Barke', a high quality malting variety. Roots were grown
for two days on filter paper at room temperature. Cloning
sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA).
NOTE: Due to a cloning artefact caused by the kit, in most

```

```

/clone_lib="HP"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA). Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable. Average insert size is
850 bp"

```

ORIGIN

```

Alignment Scores:
Pred. No.: 3,97e-25 Length: 643
Score: 253.00 Matches: 44
Percent Similarity: 90.74% Conservative: 5
Best Local Similarity: 81.48% Mismatches: 5
Query Match: 84.90% Indels: 0
DB: 6 Gaps: 0

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US-10-666-642-194_COPY_111_164 (1-54) x CB879380 (1-643)

```

QY 1 AspGlyPheLysTrpArgLysTyrgLyLysSerValLysAsnAsnLeAsnLysArg 20
|||
DB 482 GACGGCTACAAGTGGCGCAAGTACGGCAAGAAAGTCCGTCAAGAACAGCCCAAGG 541
|||
QY 21 AantTyrrLysCyseSerSerGluGlyCyseSerValLysLysArgValGluArgAspGly 40
|||
DB 542 AACTACTACCGGTGCTCGACGAAGAGGTGCGCGTGAAGAGCGGTGCGGACCGG 601
|||
QY 41 AspAspAlaAlaTyrrValIleThrThrTyrrGluGlyValHis 54
|||
DB 602 GACGACCCCGGTACGTGCTGTCACCGACCGTACGAGGCGACGCGAC 643
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```

RESULT 3

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AL503208
LOCUS AL503208 700 bp mRNA linear EST 04-JAN-2001
DEFINITION AL503208 Hordeum vulgare Barke roots Hordeum vulgare subsp. vulgare
cDNA clone HW01B17T 5', mRNA sequence.

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ACCESSION AL503208
VERSION AL503208.1 GI:12029423
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare

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```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.

```

```

REFERENCE
1 (bases 1 to 700)
Michalek,W., Weschke,W., Fleissner,K.-P. and Graner,A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W

```

```

AUTHORS Institute for Plant Genetics and Crop Plant Research
Correnstr.3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.

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Location/Qualifiers
1..700
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HW01B17T"
/tissue_type="roots"
/lab_host="XL0LR"
/clone_lib="Hordeum vulgare Barke roots"
/note="Vector: plasmid pBK-CMV; Site 1: EcoRI; Site 2:
XhoI; mRNA was made from roots of spring barley variety
'Barke', a high quality malting variety. Roots were grown
for two days on filter paper at room temperature. Cloning
sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA).
NOTE: Due to a cloning artefact caused by the kit, in most

```

FEATURES

source

chamber, excised above the soil level, and the plants were placed in a 100 ppm solution of auxin for 24 hours prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Alignment Scores:	8.67e-25	Length:	549
Pred. No.:	250.00	Matches:	43
Score:	90.74%	Conservative:	6
Percent Similarity:	79.63%	Mismatches:	5
Best Local Similarity:	83.89%	Indels:	0
Query Match:	2	Gaps:	0
DB:			

US-10-666-642-194 COPY 111 164 (1-54) x BF009428 (1-549)

QY	1	AspGlyPheLys	TrpArgLys	TyrGlyLys	ValSerVal	LysAspAsn	ValLeuAsn	Arg	20
DB	370	GATGATATTAAT	TGATGAGGAAT	ATCGGAAGAAG	CATGATGAAG	CAATCCCA	CCCCCAGG		429
QY	21	AsnTyrTyrLys	CysSerSer	GluGlyCys	SerVal	LysLysArg	ValGluArg	AspGly	40
DB	430	AACTACTACAC	TGTTTCAGGT	GAAGGATG	CAATGTGAAG	AAAGGGT	GGAAGAGACAGG		489
QY	41	AspAspAla	AlaTyrVal	LeuThrThr	TyrGluGly	ValHis		54	
DB	490	GATGACTCGAAC	TATGTGTTTAA	CAACGTAC	CACGGTGTCCAC			531	

RESULT 6				
BU547499/c				
LOCUS	BU547499	634 bp	mRNA	linear EST 16-SEP-2002
DEFINITION	GM880011A2OA06	Gm-r1088	Glycine max cDNA clone Gm-r1088-4620 3'	
			mRNA sequence.	

ACCESSION BU547499
VERSION BU547499.1 GI:22930360
KEYWORDS EST.

RECORDS	SOURCE	ORGANISM
ESI.	Glycine max (soybean)	
	Glycine max	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.	

22 pages: 1 (pages 1 to 634)

REFERENCE
Vodkin, L., Shobmaker, R., Keim, P., Retzel, E., Khanna, A., Shealy, R.,
Clough, S., Thibaud-Nissen, F., Coryell, V., Erpeliding, J., Raph, C.,
Shoop, E., Stromvik, M., Schwetzer, P., Gong, G. and Liu, L.
A Functional Genomics Program for Soybean (NSF 9872565) (2002)
Unpublished (2002)

JOURNAL
COMMENT
Other ESTs: BF009428 corresponding to Gm-cl064-248
(5')

Contract: 0007028 corresponding to 0007028 (5)
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics

University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147

Fax: (217) 333-4582
Email: l-vodkin@uiuc.edu
Insert Length: 634 Std Error: 0.00
Plate: GM880013A20 row: A column: 06
Seq primer: 5'-TTTTTTTTTTTTTTTTTT(A/C/G)-3'
High quality sequence stop: 634.

FEATURES

/mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="Gm-r1088-4620"
 /clone_lib="Gm-r1088"
 /note="The library Gm-r1088 is a sequence-driven, reracked set of 9,216 low redundancy clones selected from cDNA libraries from various tissues and stages of development of soybean that consists of 2,706 cDNAs from germinating cotyledons (source library Gm-cl027); 1,355 cDNAs from immature seed coats (libraries Gm-cl019 and Gm-cl023); 917 cDNAs from tissue culture derived somatic embryos (source libraries Gm-cl036 and Gm-cl075); 3,275 cDNAs from germinating seedlings, shoot tips, or leaves exposed to various stresses (source libraries Gm-cl064, Gm-cl065, Gm-cl066, and Gm-cl067; and Gm-cl068); and 963 cDNAs from young leaves exposed to bacterial and fungal pathogens (source libraries Gm-cl072, Gm-cl073, and Gm-cl074). The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1088 and the cDNA clones of the reracked Gm-r1088 library were then sequenced at the 3' end. The unigene selection and 3' sequencing was funded by NSF Plant Genome project #9872565 (<http://soybean.genomics.crosci.uiuc.edu/>) as part of creation of a low redundancy soybean cDNA set. The source cDNA libraries were constructed by the laboratories of Lila Vookin, University of Illinois, Randy Shoemaker, Iowa State University, and Paul Keim, Northern Arizona University as part of the Public EST project, <http://129.186.26.94/soybeanest.html>. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, <http://web.ahc.umn.edu/biodata/nfsoc/>. Reracking and 3' sequencing were conducted by services of the University of Illinois Keck Center for Comparative and Functional Genomics <http://www.biotech.uiuc.edu/keck.htm>. Note: The corresponding 5' EST from each clone in the Gm-r1088 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST.'

ORIGIN

Alignment Scores:		
Pred. No.:	1.03e-24	Length:
Score:	250.00	Matches:
Percent Similarity:	90.74%	Conservative:
Best Local Similarity:	79.63%	Mismatches:
Query Match:	83.89%	Indels:
DB:	5	Gaps:

US-10-666-642-194 COPY 111 164 (1-54) x BU547499 (1-634)

Qy 1 AspGlyPheLysTrpArgLysTyrGlyValLysSerValLysAsnAsnIleAsnLysArg 20
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Dd 473 GATGGATATAAATGGAGGAATACGGAGAAGAAGACAGTGNAGACAATCCCAACCCAAGG 414

Qy 21 AsnTyrTrpLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
 413 AACTACTCAAGTGTTCAGGTGAAGGATGCAATGTGAAGAAAGGGTGGAAAGACAGG 354
 Db

Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
 |||||:::|||||:::|||||:::|||||:::|||||
Db 353 GATGACTCGAACTATGTTTTAAACAACGTACGACGGTGTCAC 312

RESULT 7

BI209002

LOCUS	BI209002	671 bp	mRNA	linear	EST 11-JUL-2001
DEFINITION	EST527042	ctos	Lycopersicon esculentum	cdna clone	ctosL8F24 5' end,
					mRNA sequence.

VERSION BI209002.1 GI:14686726
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 671)
AUTHORS van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R., Ronning, C. and Tanksley, S.
TITLE Generation of ESTs from Tomato Suspension Cultures
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>.
FEATURES source
 1..671
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496, E6203"
 /db_xref="taxon:4081"
 /clone="cTOS18r24"
 /tissue_type="suspension cultures"
 /lab_host="SOLR"
 /clone_lib="cTOS"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Suspension cultures of L.esculentum E6203 were grown in Murashige and Skoog based medium, supplemented with 1% coconut milk (filter sterilized and added after autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8). Fresh medium was added every 7 days, and cultures were grown at 25 C, with 12hrs of light and continuous shaking."
ORIGIN
 Alignment Scores:
 Pred. No.: 1..24 Length: 671
 Score: 250.00 Matches: 44
 Percent Similarity: 88.89% Conservative: 4
 Best Local Similarity: 81.48% Mismatches: 6
 Query Match: 83.89% Indels: 0
 DB: 4 Gaps: 0
 US-10-666-642-194_COPY_111_164 (1-54) x BI209002 (1-671)
 Qy 1 AspGlyPheLysTrpArgLysTrpGlyLysSerValLysAsnAsnLysArg 20
 Db |||||
 300 GATGGATTAAATGAGGAAATATGCAAAAAGATGGTCAAGATAATCCAAATCCAAGG 359
 Qy 21 AsnTyrTrpLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
 Db |||||
 360 AATTACTACAAATGTTCAAGTGGGGGATGCAATGGAAGAAAGAGTAGAAGGACAAAT 419
 Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
 Db |||||
 420 AAAGATTCAAGCTATGCTACTACTACTACTATGAGGGATTCCAC 461
RESULT 8
 BQ515840/c 412 bp mRNA linear EST 07-MAR-2003
LOCUS BQ515840
DEFINITION EST623255 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMU36 3', end, mRNA sequence.
ACCESSION BQ515840
VERSION BQ515840.1 GI:21374709
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 412)
AUTHORS Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karanycheva, S.A.
TITLE Generation of a set of potato cDNA clones for microarray analyses
JOURNAL Unpublished (2002)
COMMENT Other ESTs: EST623254
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL: <http://genome.arizona.edu/orders/>
 Seq primer: T7.
FEATURES source
 1..412
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec or Binjite"
 /db_xref="taxon:4113"
 /clone="STMU36"
 /tissue_type="mixed tissues"
 /lab_host="SOLR"
 /clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."
ORIGIN
 Alignment Scores:
 Pred. No.: 8..47e-25 Length: 412
 Score: 249.00 Matches: 43
 Percent Similarity: 90.74% Conservative: 6
 Best Local Similarity: 79.63% Mismatches: 5
 Query Match: 83.56% Indels: 0
 DB: 5 Gaps: 0
 US-10-666-642-194_COPY_111_164 (1-54) x BQ515840 (1-412)
 Qy 1 AspGlyPheLysTrpArgLysTrpGlyLysSerValLysAsnAsnLysArg 20
 Db |||||
 406 GATGGATTAAATGAGGAAATATGCAAAAAGATGGTCAAGATAATCCAAATCCAAGG 347
 Qy 21 AsnTyrTrpLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
 Db |||||
 346 AATTACTACAAATGTTCAAGTGGGAGGATGCAATGGAAGAAAGAGTAGAAGGACAAAT 287
 Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
 Db |||||
 286 GAAGATTCAAGCTATGCTACTACTACTACTATGAGGGATTCCAC 245
RESULT 9
 BQ515840/c 418 bp mRNA linear EST 30-APR-2003
LOCUS BQ515840
DEFINITION EST536507 P. infestans-challenged potato leaf, compatible reaction Solanum tuberosum cDNA clone PPCB103 5' sequence, mRNA sequence.
ACCESSION BQ515840
VERSION BQ515840.1 GI:15258436
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 418)
AUTHORS Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemiango, A., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E. and Baker, B.
TITLE Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction

REFERENCE 1 (bases 1 to 412)
AUTHORS Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karanycheva, S.A.
TITLE Generation of a set of potato cDNA clones for microarray analyses
JOURNAL Unpublished (2002)
COMMENT Other ESTs: EST623254
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL: <http://genome.arizona.edu/orders/>
 Seq primer: T7.
FEATURES source
 1..412
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec or Binjite"
 /db_xref="taxon:4113"
 /clone="STMU36"
 /tissue_type="mixed tissues"
 /lab_host="SOLR"
 /clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."
ORIGIN
 Alignment Scores:
 Pred. No.: 8..47e-25 Length: 412
 Score: 249.00 Matches: 43
 Percent Similarity: 90.74% Conservative: 6
 Best Local Similarity: 79.63% Mismatches: 5
 Query Match: 83.56% Indels: 0
 DB: 5 Gaps: 0
 US-10-666-642-194_COPY_111_164 (1-54) x BQ515840 (1-412)
 Qy 1 AspGlyPheLysTrpArgLysTrpGlyLysSerValLysAsnAsnLysArg 20
 Db |||||
 406 GATGGATTAAATGAGGAAATATGCAAAAAGATGGTCAAGATAATCCAAATCCAAGG 347
 Qy 21 AsnTyrTrpLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
 Db |||||
 346 AATTACTACAAATGTTCAAGTGGGAGGATGCAATGGAAGAAAGAGTAGAAGGACAAAT 287
 Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
 Db |||||
 286 GAAGATTCAAGCTATGCTACTACTACTACTATGAGGGATTCCAC 245
RESULT 9
 BQ515840/c 418 bp mRNA linear EST 30-APR-2003
LOCUS BQ515840
DEFINITION EST536507 P. infestans-challenged potato leaf, compatible reaction Solanum tuberosum cDNA clone PPCB103 5' sequence, mRNA sequence.
ACCESSION BQ515840
VERSION BQ515840.1 GI:15258436
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 418)
AUTHORS Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemiango, A., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E. and Baker, B.
TITLE Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction

This sequence has been generated in the framework of the french plant genomics programme "Genoplante" (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr/>.

FEATURES

source
1..466
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="mixture"
/db_xref="taxon:4577"
/clone_lib="Genetag2"

ORIGIN

Alignment Scores:
Pred. No.: 9.83e-25 Length: 466
Score: 249.00 Matches: 44
Percent Similarity: 88.89% Conservative: 4
Best Local Similarity: 81.48% Mismatches: 6
Query Match: 83.56% Indels: 0
DB: 6 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x CD967539 (1-466)

Qy 1 AspGlyPheLysTrpArgLysTyrgLysLysSerValLysAsnAsnLysArg 20
|||
Db 11 GACGATTCAAGTGGAGGAGTACGGGAAGAGCGGTCAAGACAGCCCAATCCAAGG 70
|||
Qy 21 AsnTyrtYrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
|||
Db 71 AACTACTACCGCTGCTCGTGGAGGGCTGCGGTGAAGAGCGGTGGAGAGGACCGC 130
|||
Qy 41 AspAspAlaAlaTyrrValIleThrThrTyrgLuglyValHis 54
|||
Db 131 GACGACCCCGCTACGTCAATCACCACCTACGACGCGGTCCAC 172
|||

RESULT 12

AW744840
LOCUS
DEFINITION LG1_384_F02_g1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
sequence.
AW744840
VERSION
AW744840.1 GI:7658644
KEYWORDS
EST.
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 497)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.

Seq primer: T7
High quality sequence start: 45
High quality sequence stop: 497
POLYA=Yes.

Location/Qualifiers
1..497
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/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2:

FEATURES

source
1..497
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2:

ORIGIN

Alignment Scores:
Pred. No.: 1.06e-24 Length: 497
Score: 249.00 Matches: 44
Percent Similarity: 88.89% Conservative: 4
Best Local Similarity: 81.48% Mismatches: 6
Query Match: 83.56% Indels: 0
DB: 2 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x AW744840 (1-497)

Qy 1 AspGlyPheLysTrpArgLysTyrgLysLysSerValLysAsnAsnLysArg 20
|||
Db 43 GATGATTCAAGTGGAGGAGTATGGGAAGAGCGGTCAAGACAGCCCAATCCAAGG 102
|||
Qy 21 AsnTyrtYrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
|||
Db 103 AACTACTACCGCTGCTCGGAGGGCTGCGGTGAAGAGCGGTGGAGAGGACCGC 162
|||
Qy 41 AspAspAlaAlaTyrrValIleThrThrTyrgLuglyValHis 54
|||
Db 163 GACGACCCCGTACGTCAATCACCACCTACGACGCGGTCCAC 204
|||

RESULT 13

BG049241
LOCUS
DEFINITION OVI_17_D05_g1_A002 Ovary 1 (OVI) Sorghum bicolor cDNA, mRNA
sequence.
BG049241
VERSION
BG049241.1 GI:12500807
KEYWORDS
EST.
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 501)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and
Pratt,L.H.
An EST database from Sorghum: ovaries of varying immature stages
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.

Seq primer: PolyTMix
High quality sequence start: 246
High quality sequence stop: 498
POLYA=No.

Location/Qualifiers
1..501
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Ovary 1 (OVI)"
/note="Organ: Mix of ovaries of varying immature stages
from 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
from poly-A RNA in the cloning vector lambda Zap II.
Clones to be sequenced were prepared by mass excision."

FEATURES

source
1..501
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Ovary 1 (OVI)"
/note="Organ: Mix of ovaries of varying immature stages
from 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
from poly-A RNA in the cloning vector lambda Zap II.
Clones to be sequenced were prepared by mass excision."

ORIGIN

Alignment Scores:

```

Pred. No.: 1,07e-24 Length: 501
Score: 249.00 Matches: 44
Percent Similarity: 88.89% Conservatives: 4
Best Local Similarity: 81.48% Mismatches: 6
Query Match: 83.56% Indels: 0
DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x BG049241 (1-501)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20
|||||
DQ 117 CATGATTCAATGGAGGAAGTATGGGAAGAGGCTGTCAAGAACAGCCCAATCCAAAGG 176
|||||

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysArgValGluArgAspGly 40
|||||
DQ 177 AACTACTACCGTGTCTGCGGAGGCGCTCGCGGTGAAGAACGGGTGGAGAGGACCGC 236
|||||

QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
|||||
DQ 237 GACGACCCCGCTACGTCTATCACCACCTACGACGCGGTCCAC 278
|||||

RESULT 14
BE216050
LOCUS
DEFINITION
HVCED0009E04f Hordeum vulgare seedling green leaf EST library
HVCEDNA0005 (Blumeria challenged) Hordeum vulgare subsp. vulgare
CDNA clone HV_CEB0009E04f, mRNA sequence.
ACCESSION
BE216050
VERSION
KEYWORDS
SOURCE
Hordeum vulgare subsp. vulgare
ORGANISM
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 584)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
Friesch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J.,
Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla6) seedling
leaf cDNA library
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 325
Seq primer: AATTACCTCTACTAAAGG
High quality sequence stop: 556.
Location/Qualifiers
1..584
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Cil16151 (Mla6)"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HV_CEB0009E04f"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HVCEDNA0005 (Blumeria challenged)"
/note="Vector: lambdaZAP; Site.1: EcoRI; Site.2: XhoI;
C.I. 16151 (Mla6) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate 5874
(AvrMla6) of Blumeria graminis f. sp. hordei, and leaves
were harvested 20 and 24 hr post-inoculation and snap
frozen; uninoculated leaves were harvested 20 hr
post-inoculation (Wei, Wise). In the TJ Close lab at the

```

University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Friesch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Friesch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

ORIGIN

```

Alignment Scores:
Pred. No.: 1,29e-24 Length: 584
Score: 249.00 Matches: 43
Percent Similarity: 88.89% Conservatives: 5
Best Local Similarity: 79.83% Mismatches: 6
Query Match: 83.56% Indels: 0
DB: 2 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x BE216050 (1-584)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20
|||||
DQ 377 GACGCTACAAAGTCGCGCAAGTCAAGCAAGTCCGTCGAAGACAGCCCAACCCCAAGG 436
|||||

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysArgValGluArgAspGly 40
|||||
DQ 437 AACTACTACCGTGTCTGCGGAGGCGTGCACGTGAAGACGGGTGGAGCGGACCGG 496
|||||

QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
|||||
DQ 497 GACGATCGCGGTACGTGGTGACCAACGTCACGAGGCGACGCAC 538
|||||

```

```

RESULT 15
BM328984
LOCUS
DEFINITION
PIC1_31_H12-gl_A002 Pathogen-infected compatible 1 (PIC1) Sorghum
bicolor cDNA, mRNA sequence.
ACCESSION
BM328984
VERSION
BM328984.1 GI:18068121
KEYWORDS
EST.
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 610)
Cordonnier-Pratt,M.-M., Gingle,A., Fang,G.C., Dean,R., Wing,R.,
Sudman,M. and Pratt,L.H.
An EST database from Sorghum: plants infected with a compatible
pathogen
Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20. Three-prime sequences, which are obtained with PolyTWix or

```

T7 sequencing primer, are presented as the reverse complement.

Seq primer: T7
High quality sequence start: 20
High quality sequence stop: 610
POLYA=Yes.

FEATURES

source
Location/Qualifiers
1..610
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/issue_type="Leaves"
/dev_stage="4-week-old seedlings infected with Colletotrichum graminicola"
/clone_lib="Pathogen-infected compatible 1 (PIC1)"
/note="Vector: pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; Four-week-old sorghum seedlings were sprayed with spore suspension prepared from 3-week-old FRM421, a sorghum isolate of the anthracnose pathogen Colletotrichum graminicola. Inoculated plants were kept in a 25 C dark growth chamber with 100% relative humidity for 24 hr, followed by 12/12 hr of light/dark cycle at 25 C with 90% relative humidity for another 24 hr. All leaves were harvested and quick frozen with liquid nitrogen and stored in a -80 C freezer. The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."

ORIGIN

Alignment Scores:
Pred. No.: 1.36e-24 Length: 610
Score: 249.00 Matches: 44
Percent Similarity: 88.89% Conservative: 4
Best Local Similarity: 81.48% Mismatches: 6
Query Match: 83.56% Indels: 0
DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x BM328984 (1-610)

Qy 1 AspGlyPheLysTyrArgLysTyrGlyLysLysSerValLysAsnAsnIleAsnLysArg 20
Db 133 GATGGATTCAATGAGGAAGTATCGGAAGAGGCTGTCAAGAACAGCCCAATCCAAGG 192
Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
Db 193 AACTACTACCGCTGCTCGTGGAGGGCTGCGGCGTGAAGAGCGGGTGGAGAGGACCGC 252
Qy 41 AspAspAlaAlaTyrValIleThrTyrThrTyrGluGlyValHis 54
Db 253 GACGACCCCGCTAGCTCATCACCACTACGACGCGGTCCAC 294

Search completed: August 26, 2005, 01:46:02
Job time : 2312 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 25, 2005, 18:08:19 ; Search time 391 Seconds
(without alignments)

817.560 Million cell updates/sec

Title: US-10-666-642-194_COPY_111_164

Perfect score: 298

Sequence: 1 DGFKWKYKGVKSNINKR.....RVERDGDAAAYVITTYEGVH 54

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q/cgn2_1/USPRO_spool/US10666642/runat_25082005_130052_24846/app_query.fasta_1.199
-DB=N Geneseq_16Dec04 -QMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10666642 @CGN 1 1 644 @runat_25082005_130052_24846 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREAS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_16Dec04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	298	100.0	585	12 ADO02392	Ado02392 Thalecres
2	298	100.0	585	12 ADO61726	Ado61726 Thalecres
3	298	100.0	1917	3 AAC49725	Aac49725 Arabidops
4	250	83.9	740	12 ADO63551	Ado63551 Thalecres
5	249	83.6	823	12 ADO03201	Ado03201 Corn orth

6	249	83.6	823	12 ADO62507	Ado62507 Thalecres
7	249	83.6	1663	12 ADI43068	Adi43068 Plant tra
8	249	83.6	1663	12 ADO03208	Ado03208 Corn orth
9	248	83.2	680	12 ADO03200	Ado03200 Corn orth
10	248	83.2	680	12 ADO62506	Ado62506 Thalecres
11	248	83.2	743	12 ADO03199	Ado03199 Corn orth
12	248	83.2	743	12 ADO62505	Ado62505 Thalecres
13	247	82.9	974	12 ADO03196	Ado03196 Soybean o
14	247	82.9	974	12 ADO62502	Ado62502 Thalecres
15	244	81.9	1696	12 ADI43067	Adi43067 Plant tra
16	244	81.9	1696	12 ADO03207	Ado03207 Corn orth
17	243	81.5	834	12 ADO03202	Ado03202 Corn orth
18	243	81.5	834	12 ADO62508	Ado62508 Thalecres
19	242	81.2	825	12 ADI43066	Adi43066 Plant tra
20	242	81.2	825	12 ADO03203	Ado03203 Rice orth
21	239	80.2	1235	12 ADO03195	Ado03195 Soybean o
22	239	80.2	1235	12 ADO62501	Ado62501 Thalecres
23	232	77.9	999	12 ADI43069	Adi43069 Plant tra
24	232	77.9	999	12 ADO03209	Ado03209 Corn orth
25	230	77.2	748	6 ABK65246	Abk65246 Arabidops
26	230	77.2	748	9 ACD98373	Acd98373 A. thalia
27	230	77.2	748	10 ADD29972	Add29972 Plant yie
28	230	77.2	748	12 ADI41790	Adi41790 Plant tra
29	230	77.2	748	12 ADO02394	Ado02394 Thalecres
30	197	66.1	444	3 AAC45051	Aac45051 Arabidops
31	197	66.1	548	3 AAC35279	Aac35279 Arabidops
32	197	66.1	569	3 AAC48380	Aac48380 Arabidops
33	197	66.1	624	3 AAC38694	Aac38694 Arabidops
34	197	66.1	724	9 ADA15508	Ada15508 DNA encod
35	197	66.1	724	9 ACD98365	Acd98366 A. thalia
36	197	66.1	724	12 ADO01672	Ado01672 Thalecres
37	197	66.1	1306	10 ADD31000	Add31000 Plant yie
38	197	66.1	1306	12 ADI44148	Adi44148 Plant tra
39	197	66.1	1306	12 ADO61750	Ado61750 Thalecres
40	195	65.4	1182	6 ABZ13876	Abz13876 Arabidops
41	195	65.4	1182	8 ADA68247	Ada68247 Arabidops
42	195	65.4	1398	9 ADA15532	Ada15532 DNA encod
43	195	65.4	1398	12 ADO01670	Ado01670 Thalecres
44	195	65.4	1462	9 ADB23121	Adb23121 Environme
45	195	65.4	1589	3 AAC40213	Aac40213 Arabidops

ALIGNMENTS

RESULT 1
ADO02392
ID ADO02392 standard; cDNA; 585 BP.
XX
AC ADO02392;
XX
DT 01-JUL-2004 (first entry)
XX
DE Thalecres transcription factor cDNA #403.
XX

Thalecres; transcription factor; ss, gene; plant; transgenic;
abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;
phosphate limitation; potassium limitation; nitrogen limitation;
hormone sensitivity; disease resistance; sugar sensing; seed germination;
flowering; inflorescence architectural change;
meristem cell differentiation; phyllotaxy; apical dominance;
trichome development; seed development; premature senescence;
delayed senescence; lethality; necrosis; plant size; leaf morphology;
seed morphology; secondary metabolism; light response; shade avoidance.

Arabidopsis thaliana.

US2004045049-A1.

04-MAR-2004.

10-APR-2003; 2003US-00412699.

13-SEP-1999; 99US-00394519.

PR 21-JAN-2000; 2000US-00489376.
 PR 17-FEB-2000; 2000US-00506720.
 PR 22-MAR-2000; 2000US-00532591.
 PR 22-MAR-2000; 2000US-00533028.
 PR 22-MAR-2000; 2000US-00533030.
 PR 22-MAR-2000; 2000US-00533392.
 PR 22-MAR-2000; 2000US-00533648.
 PR 06-APR-2000; 2000WO-US009448.
 PR 16-NOV-2000; 2000US-00713994.
 PR 17-MAR-2001; 2001US-00819142.
 PR 17-APR-2001; 2001US-00837444.
 PR 30-JAN-2002; 2002US-00958131.
 PR 14-JUN-2002; 2002US-00171468.
 PR 09-AUG-2002; 2002US-00225066.
 PR 09-AUG-2002; 2002US-00225067.
 PR 09-AUG-2002; 2002US-00225068.
 PR 17-DEC-2002; 2002US-0434166P.
 PR 25-FEB-2003; 2003US-00374780.
 XX
 PA (ZHAN/) ZHANG J.
 PA (FROM/) FROMM M E.
 PA (HEAR/) HEARD J E.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUN P E.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KENDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMAHA R S.
 PA (PILG/) PILGRIM M L.
 PA (CREE/) CREELMAN R A.
 PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KUMI/) KUMIMOTO R.
 PA (SHER/) SHERMAN B K.
 XX
 PI Zhang J, Fromm ME, Riechmann JL, Adam LJ, Broun PE;
 PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS;
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
 PI Sherman BK;
 XX
 DR WPI; 2004-225755/21.
 DR P-PSDB; ADO02393.
 XX
 XX New transgenic plant, useful in developing phenotypes with altered or
 PT improved characteristics or traits.
 PT
 PS Claim 1; SEQ ID NO 805; 213pp; English.
 PS
 CC The invention relates to a transgenic plant comprising a recombinant
 CC polynucleotide having a polynucleotide sequence or its complementary
 CC sequence comprising a sequence encoding a polypeptide, that initiates
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
 CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588
 CC -ADO03527 or ADO03530-ADO03559. Also included are using a transgenic
 CC plant to grow a progeny plant, an expression cassette (comprising a
 CC constitutive, inducible or tissue-specific promoter and a recombinant
 CC polynucleotide described above), a host cell comprising the expression
 CC cassette, producing a modified plant having a modified trait, identifying
 CC a factor that is modulated by or interacts with a polypeptide encoded by
 CC the polynucleotide sequence and identifying at least one downstream
 CC polynucleotide sequence that is subject to a regulatory effect of any of
 CC the polypeptides encoded by the polynucleotide described above. The
 CC transgenic plant is useful for producing a plant that has an altered
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to
 CC salt, tolerance to phosphate limitation, tolerance to potassium
 CC limitation, decreased sensitivity to nitrogen limitation), altered
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered
 CC response to ethylene, disease resistance, altered susceptibility to

CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to
 CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered
 CC susceptibility to Sclerotinia, altered sugar sensing, improved seed
 CC germination and seedling vigor, early flowering, late flowering, extended
 CC period of flowering, an inflorescence architectural change, a change in
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell
 CC differentiation, altered phyllotaxy, altered branching pattern, reduced
 CC apical dominance, reduced trichome density, ectopic trichome development,
 CC altered trichome development, altered stem morphology, increased root
 CC growth, increased root hairs, altered stem development, altered cell
 CC proliferation/cell differentiation, premature senescence, delayed
 CC senescence, lethality, increased necrosis, an increase in seedling or
 CC plant size, decreased plant size, a change in leaf morphology, increased
 CC altered leaf development, increased leaf size and mass, glossy leaves,
 CC leaf cell expansion, change in seed morphology, altered seed coloration,
 CC increased seed size, decreased seed size, altered seed shape, change in
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenly lipid
 CC content, increased leaf insoluble sugars, decreased leaf insoluble
 CC sugars, an alteration of leaf glucosinolate content, change in seed
 CC content, an increase in seed oil content, decrease in seed oil
 CC content, increase in seed fatty acid content, decrease in seed fatty acid
 CC content, increase in seed protein content, decrease in seed protein
 CC content, alteration in seed prenly lipid content, increase in seed
 CC sterols, upregulation of genes involved in secondary metabolism, increase
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in
 CC light response or shade avoidance. The present sequence encodes a
 CC thalacress transcription factor of the invention.
 XX
 SQ Sequence 585 BP; 202 A; 95 C; 135 G; 153 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 5, 9e-34 Length: 585
 Score: 298.00 Matches: 54
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0
 US-10-666-642-194_COPY_111_164 (1-54) x ADO02392 (1-585)
 QY 1 AspGlyPheLysTrpArgLysTyrglyLysLysSerValLysAsnAsnLysArg 20
 Db 331 GATGGTTTAAATCGAGGAGTATGGCAAGAAATCTGTCAAAAACACATTAACAAGAGG 390
 QY 21 AsnTyrrTyrrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
 Db 391 AATTACTACAAATGCTCAAGTGAAGAGGTTCGCGTGAAGAGAGGGTAGAGAGATGGT 450
 QY 41 AspAspAlaAlaTyrrValIleThrThrTyrrGluGlyValHis 54
 Db 451 GACGATGCGAGCTTATGTATTAATACACATATGAGGAGTCCAT 492
 RESULT 2
 ADO61726
 ID ADO61726 standard; DNA; 585 BP.
 XX
 AC ADO61726;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Transcription factor G1274 coding sequence, SEQ ID 193.
 XX
 KW Plant; transcription factor; transgenic plant; abiotic stress tolerance;
 KW osmotic stress tolerance; cold tolerance; heat tolerance;
 KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
 KW glyphosate resistance; flowering; fertility; seed development; ds.
 OS Arabidopsis thaliana.
 XX
 FN WO2004031349-A2.
 XX
 PD 15-APR-2004.

XX 18-SEP-2003; 2003WO-US030292.
XX 18-SEP-2002; 2002US-0411837P.
XX 17-DEC-2002; 2002US-0434156P.
XX 24-APR-2003; 2003US-0465809P.
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
XX Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;
XX Riechmann JL, Haake V, Dubell AN, Keddle JS, Sherman BK;
XX WPI; 2004-330163/30.
XX P-ESDB; ADO61727.
XX New recombinant polynucleotide encoding transcription factor
XX polypeptides, useful for producing transgenic plants with advantageous
XX properties compared to a reference plant.
XX Claim 1; SEQ ID NO 193; 510pp; English.
XX The present invention relates to novel plant transcription factor
XX proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
XX sequences can be used to produce transgenic plants, which overexpress
XX (II), where the transgenic plant has an altered trait as compared to a
XX non-transgenic plant or wild-type plant. The transgenic plant comprises
XX an altered trait selected from increased tolerance to abiotic stress,
XX increased tolerance to osmotic stress, increased tolerance to cold,
XX increased germination in cold, increased tolerance to heat, increased
XX germination in heat, increased tolerance to freezing conditions,
XX increased tolerance to low nitrogen conditions, increased tolerance to
XX low phosphate conditions, increased tolerance to disease, including
XX fungal disease and particularly Erysiphe, Fusarium and Botrytis,
XX increased tolerance to multiple fungal pathogens, increased resistance to
XX glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
XX increased sensitivity to ACC, altered sugar sensing, increased tolerance
XX to sugars, altered carbon/nitrogen sensing, early flowering, late
XX flowering, altered flower meristem development, altered branching pattern,
XX fertility, altered shoot meristem development, altered branching pattern,
XX altered stem morphology, altered vascular tissue structure, reduced
XX apical dominance, altered trichome density, altered trichome development,
XX altered trichome structure, altered root development, altered shade
XX avoidance, altered seed development, altered seed ripening, altered seed
XX germination, slow growth, fast growth, altered cell differentiation,
XX altered cell proliferation, altered cell expansion, altered phase change,
XX altered senescence, abnormal embryo development, altered programmed cell
XX death, lethality when overexpressed, altered necrosis patterns, increased
XX plant size, increased biomass, large seedlings, dwarfed plants, dark
XX green leaves, change in leaf shape, increased leaf size and mass, light
XX green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
XX altered seed coloration, altered seed size, altered seed shape, large
XX seed, increased leaf wax, increased leaf fatty acids, altered seed oil
XX content, altered seed protein content, altered seedprenyl content,
XX altered leaf prenyl lipid content, increased anthocyanin levels, and
XX decreased anthocyanin levels. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 585 BP; 202 A; 95 C; 135 G; 153 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 59e-34 Length: 585
Score: 298.00 Matches: 54
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-666-642-194_COPY_111_164 (1-54) x ADO61726 (1-585)
Qy 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnLysArg 20
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Db 331 GATGGTTTTAAATGGAGGAAGTATGGCAAGAAATCTGTCAAAAACACATTAAACAGAGG 390
Qy 21 AsnTyrTrpLysCySerSerGluGlyCySerValLysValGluArgAspGly 40
|||||
Db 391 AATTACTACAAATGCTCAAGTGAAGGTTGCTCGGTGAAGAAGAGGGGTAGAGAGATGGT 450
Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
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Db 451 GACGATGCAGCTTATGTATTAATACAACATATGAAGGAGTCCAT 492
RESULT 3
AAC49725
ID AAC49725 standard; DNA; 1917 BP.
XX
AC AAC49725;
XX
DT 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 62208.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128214P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999;	99US-0138847P.	PR 10-AUG-1999;	99US-0148171P.
PR 14-JUN-1999;	99US-0139119P.	PR 11-AUG-1999;	99US-0148319P.
PR 16-JUN-1999;	99US-0139452P.	PR 12-AUG-1999;	99US-0148341P.
PR 16-JUN-1999;	99US-0139453P.	PR 13-AUG-1999;	99US-0148565P.
PR 17-JUN-1999;	99US-0139492P.	PR 13-AUG-1999;	99US-0148684P.
PR 18-JUN-1999;	99US-0139454P.	PR 16-AUG-1999;	99US-0149368P.
PR 18-JUN-1999;	99US-0139455P.	PR 17-AUG-1999;	99US-0149175P.
PR 18-JUN-1999;	99US-0139456P.	PR 18-AUG-1999;	99US-0149436P.
PR 18-JUN-1999;	99US-0139457P.	PR 20-AUG-1999;	99US-0149722P.
PR 18-JUN-1999;	99US-0139458P.	PR 20-AUG-1999;	99US-0149723P.
PR 18-JUN-1999;	99US-0139459P.	PR 20-AUG-1999;	99US-0149929P.
PR 18-JUN-1999;	99US-0139460P.	PR 23-AUG-1999;	99US-0149902P.
PR 18-JUN-1999;	99US-0139461P.	PR 23-AUG-1999;	99US-0149930P.
PR 18-JUN-1999;	99US-0139462P.	PR 25-AUG-1999;	99US-0150566P.
PR 18-JUN-1999;	99US-0139463P.	PR 26-AUG-1999;	99US-0150884P.
PR 18-JUN-1999;	99US-0139750P.	PR 27-AUG-1999;	99US-0151065P.
PR 18-JUN-1999;	99US-0139763P.	PR 27-AUG-1999;	99US-0151066P.
PR 21-JUN-1999;	99US-01398117P.	PR 27-AUG-1999;	99US-0151080P.
PR 22-JUN-1999;	99US-0139899P.	PR 30-AUG-1999;	99US-0151303P.
PR 23-JUN-1999;	99US-0140353P.	PR 31-AUG-1999;	99US-0151438P.
PR 23-JUN-1999;	99US-0140354P.	PR 01-SEP-1999;	99US-0151930P.
PR 24-JUN-1999;	99US-0140695P.	PR 07-SEP-1999;	99US-0152363P.
PR 28-JUN-1999;	99US-0140823P.	PR 10-SEP-1999;	99US-0153070P.
PR 29-JUN-1999;	99US-0140991P.	PR 13-SEP-1999;	99US-0153758P.
PR 30-JUN-1999;	99US-0141287P.	PR 15-SEP-1999;	99US-0154018P.
PR 01-JUL-1999;	99US-0141842P.	PR 16-SEP-1999;	99US-0154039P.
PR 01-JUL-1999;	99US-0142154P.	PR 20-SEP-1999;	99US-0154779P.
PR 02-JUL-1999;	99US-0142055P.	PR 22-SEP-1999;	99US-0155139P.
PR 06-JUL-1999;	99US-0142390P.	PR 23-SEP-1999;	99US-0155486P.
PR 08-JUL-1999;	99US-0142803P.	PR 24-SEP-1999;	99US-0155659P.
PR 09-JUL-1999;	99US-0142920P.	PR 28-SEP-1999;	99US-0156458P.
PR 12-JUL-1999;	99US-0142977P.	PR 29-SEP-1999;	99US-0156596P.
PR 13-JUL-1999;	99US-0143542P.	PR 04-OCT-1999;	99US-0157117P.
PR 14-JUL-1999;	99US-0143624P.	PR 05-OCT-1999;	99US-0157753P.
PR 15-JUL-1999;	99US-0144005P.	PR 06-OCT-1999;	99US-0157865P.
PR 16-JUL-1999;	99US-0144085P.	PR 07-OCT-1999;	99US-0158029P.
PR 16-JUL-1999;	99US-0144086P.	PR 08-OCT-1999;	99US-0158232P.
PR 19-JUL-1999;	99US-0144325P.	PR 12-OCT-1999;	99US-0158369P.
PR 19-JUL-1999;	99US-0144331P.	PR 13-OCT-1999;	99US-0159283P.
PR 19-JUL-1999;	99US-0144332P.	PR 13-OCT-1999;	99US-0159294P.
PR 19-JUL-1999;	99US-0144333P.	PR 13-OCT-1999;	99US-0159295P.
PR 19-JUL-1999;	99US-0144334P.	PR 14-OCT-1999;	99US-0159329P.
PR 20-JUL-1999;	99US-0144335P.	PR 14-OCT-1999;	99US-0159330P.
PR 20-JUL-1999;	99US-0144352P.	PR 14-OCT-1999;	99US-0159331P.
PR 20-JUL-1999;	99US-0144632P.	PR 14-OCT-1999;	99US-0159637P.
PR 20-JUL-1999;	99US-0144884P.	PR 14-OCT-1999;	99US-0159638P.
PR 21-JUL-1999;	99US-0144814P.	PR 18-OCT-1999;	99US-0159584P.
PR 21-JUL-1999;	99US-0145086P.	PR 21-OCT-1999;	99US-0160741P.
PR 21-JUL-1999;	99US-0145088P.	PR 21-OCT-1999;	99US-0160767P.
PR 22-JUL-1999;	99US-0145085P.	PR 21-OCT-1999;	99US-0160768P.
PR 22-JUL-1999;	99US-0145087P.	PR 21-OCT-1999;	99US-0160770P.
PR 22-JUL-1999;	99US-0145089P.	PR 21-OCT-1999;	99US-0160814P.
PR 22-JUL-1999;	99US-0145192P.	PR 21-OCT-1999;	99US-0160815P.
PR 23-JUL-1999;	99US-0145145P.	PR 22-OCT-1999;	99US-0160980P.
PR 23-JUL-1999;	99US-0145218P.	PR 22-OCT-1999;	99US-0160981P.
PR 23-JUL-1999;	99US-0145224P.	PR 22-OCT-1999;	99US-0160989P.
PR 26-JUL-1999;	99US-0145276P.	PR 25-OCT-1999;	99US-0161404P.
PR 27-JUL-1999;	99US-0145913P.	PR 25-OCT-1999;	99US-0161405P.
PR 27-JUL-1999;	99US-0145918P.	PR 25-OCT-1999;	99US-0161406P.
PR 27-JUL-1999;	99US-0145919P.	PR 26-OCT-1999;	99US-0161359P.
PR 28-JUL-1999;	99US-0145951P.	PR 26-OCT-1999;	99US-0161360P.
PR 02-AUG-1999;	99US-0146386P.	PR 26-OCT-1999;	99US-0161361P.
PR 02-AUG-1999;	99US-0146388P.	PR 28-OCT-1999;	99US-0161920P.
PR 02-AUG-1999;	99US-0146389P.	PR 28-OCT-1999;	99US-0161922P.
PR 03-AUG-1999;	99US-0147038P.	PR 28-OCT-1999;	99US-0161993P.
PR 04-AUG-1999;	99US-0147204P.	PR 29-OCT-1999;	99US-0162142P.
PR 05-AUG-1999;	99US-0147302P.		
PR 05-AUG-1999;	99US-0147192P.		
PR 06-AUG-1999;	99US-0147260P.		
PR 06-AUG-1999;	99US-0147303P.		
PR 06-AUG-1999;	99US-0147416P.		
PR 09-AUG-1999;	99US-0147493P.		
PR 09-AUG-1999;	99US-0147935P.		

Alignment Scores:

Pred. No.:

2.84e-33

Score:

298.00

Percent Similarity:

100.00%

Best Local Similarity:

100.00%

Query Match:

100.00%

Length:

1917

Matches:

54

Conservative:

0

Mismatches:

0

Indels:

0

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QY 1 AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAenLysArg 20
DB 331 GATGGTTTAAATGGAGAGATATGGCAAGAAATCTGTCAAAACAACATTAACAGG 390
QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
DB 391 AATTACTACAAATGCTCAAGTGAAGGTTGCTCGGTGAAGAAGAGGGTAGAGAGATGGT 450
QY 41 AspAspAlaLysValLleThrTyrGluGlyValHis 54
DB 451 GACGATGCAGCTTATGTAAATACAAACATATGAGGAGTCCAT 492
RESULT 4
ADO63551/C
ID ADO63551 standard; DNA; 740 BP.
XX
AC ADO63551;
XX
XX 15-JUL-2004 (first entry)
XX
DE Transcription factor G1274 orthologous sequence, SEQ ID 2018.
XX
XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;
KW osmotic stress tolerance; cold tolerance; heat tolerance;
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
KW glycosate resistance; flowering; fertility; seed development; ds.
XX
OS Lycopersicon esculentum.
XX
XX WO2004031349-A2.
XX
XX 15-APR-2004.
XX
XX 18-SEP-2003; 2003WO-US030292.
XX
XX 18-SEP-2002; 2002US-0411837P.
XX
XX 17-DEC-2002; 2002US-0434166P.
XX
XX 24-APR-2003; 2003US-0465809P.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
XX Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;
PI Riechmann JL, Haake V, Dubell AN, Keddle JS, Sherman BK;
XX
XX WPI; 2004-330163/30.
XX
XX New recombinant polynucleotide encoding transcription factor
PT polypeptides, useful for producing transgenic plants with advantageous
PT properties compared to a reference plant.
XX
XX Claim 1; SEQ ID NO 2018; 510pp; English.
XX
XX The present invention relates to novel plant transcription factor
CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
CC sequences can be used to produce transgenic plants, which overexpress
CC (II), where the transgenic plant has an altered trait as compared to a
CC non-transgenic plant or wild-type plant. The transgenic plant comprises
CC an altered trait selected from increased tolerance to abiotic stress,
CC increased tolerance to osmotic stress, increased tolerance to cold,
CC increased germination in cold, increased tolerance to heat, increased
CC germination in heat, increased tolerance to freezing conditions,
CC increased tolerance to low nitrogen conditions, increased tolerance to
CC low phosphate conditions, increased tolerance to disease, including
CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,
CC increased tolerance to multiple fungal pathogens, increased resistance to
CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
CC increased sensitivity to ACC, altered sugar sensing, increased tolerance
CC to sugars, altered carbon/nitrogen sensing, early flowering, late
CC flowering, altered flower structure, loss of flower determinacy, reduced

CC fertility, altered shoot meristem development, altered branching pattern,
CC altered stem morphology, altered vascular tissue structure, reduced
CC apical dominance, altered trichome density, altered trichome development,
CC altered trichome structure, altered root development, altered shade
CC avoidance, altered seed development, altered seed ripening, altered seed
CC germination, slow growth, fast growth, altered cell differentiation,
CC altered cell proliferation, altered cell expansion, altered phase change,
CC altered senescence, abnormal embryo development, altered programmed cell
CC death, lethality when overexpressed, altered necrosis patterns, increased
CC plant size, increased biomass, large seedlings, dwarfed plants, dark
CC green leaves, change in leaf shape, increased leaf size and mass, light
CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
CC altered seed coloration, altered seed size, altered seed shape, large
CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil
CC content, altered seed protein content, altered seedprenyl content,
CC altered leaf prenyl lipid content, increased anthocyanin levels, and
CC decreased anthocyanin levels. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 740 BP; 229 A; 131 C; 114 G; 266 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8.78e-27 Length: 740
Score: 250.00 Matches: 44
Percent Similarity: 88.89% Conservative: 4
Best Local Similarity: 81.48% Mismatches: 6
Query Match: 83.89% Indels: 0
DB: 12 Gaps: 0
US-10-666-642-194_COPY_111_164 (1-54) x ADO63551 (1-740)
QY 1 AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAenLysArg 20
DB 435 GATGGTTTAAATGGAGAGATATGGCAAAAGATGTCAGATATATCCATCCAAGG 376
QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
DB 375 AATTACTACAAATGCTCAAGTGGGGATGCAATGTGAAGAAAGAGTAGAAGGACAAT 316
QY 41 AspAspAlaLysValLleThrTyrGluGlyValHis 54
DB 315 AAAGATTCAAGCTATGTCTATTACTATTATGAAGGGGATTCAC 274
RESULT 5
ADO03201
ID ADO03201 standard; CDNA; 823 BP.
XX
AC ADO03201;
XX
XX 01-JUL-2004 (first entry)
XX
XX Corn orthologue of Thalecress transcription factor, CDNA #180.
XX
XX Corn; transcription factor; ss; gene; plant; transgenic; abiotic stress;
KW cold tolerance; heat tolerance; drought; osmotic stress;
KW phosphate limitation; potassium limitation; nitrogen limitation;
KW hormone sensitivity; disease resistance; sugar sensing; seed germination;
KW flowering; inflorescence architectural change;
KW meristem cell differentiation; phyllotaxy; apical dominance;
KW trichome development; seed development; premature senescence;
KW delayed senescence; lethality; necrosis; plant size; leaf morphology;
KW seed morphology; secondary metabolism; light response; shade avoidance.
XX
XX Zea mays.
XX
XX US2004045049-A1.
XX
XX 04-MAR-2004.
XX
XX 10-APR-2003; 2003US-00412699.
XX

PR 13-SEP-1999; 99US-00394519.
 PR 17-JAN-2000; 2000US-00489376.
 PR 21-FEB-2000; 2000US-00506720.
 PR 22-MAR-2000; 2000US-00532591.
 PR 22-MAR-2000; 2000US-00533029.
 PR 22-MAR-2000; 2000US-00533030.
 PR 22-MAR-2000; 2000US-00533392.
 PR 22-MAR-2000; 2000US-00533648.
 PR 06-APR-2000; 2000WO-US009448.
 PR 16-NOV-2000; 2000US-00713994.
 PR 27-MAR-2001; 2001US-00819142.
 PR 17-APR-2001; 2001US-00837444.
 PR 30-JAN-2002; 2002US-00958131.
 PR 14-JUN-2002; 2002US-00171468.
 PR 09-AUG-2002; 2002US-00225066.
 PR 09-AUG-2002; 2002US-00225067.
 PR 09-AUG-2002; 2002US-00225068.
 PR 17-DEC-2002; 2002US-0434166P.
 PR 25-FEB-2003; 2003US-00374780.
 XX
 PA (ZHAN/) ZHANG J.
 PA (FROM/) FROMM M E.
 PA (HEAR/) HEARD J E.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUN P E.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMAHA R S.
 PA (PILG/) PILGRIM M L.
 PA (CREE/) CREELMAN R A.
 PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KUMI/) KUMIMOTO R.
 PA (SHER/) SHERMAN B K.
 XX
 PI Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE;
 PI Pineda O, Reuber TL, Keddle JS, Yu G, Jiang C, Samaha RS;
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
 PI Sherman BK;
 XX WPI; 2004-225755/21.
 XX
 PT New transgenic plant, useful in developing phenotypes with altered or
 PT improved characteristics or traits.
 XX
 PS Claim 1; SEQ ID NO 1615; 213pp; English.
 XX
 CC The invention relates to a transgenic plant comprises a recombinant
 CC polynucleotide having a polynucleotide sequence or its complementary
 CC sequence comprising a sequence encoding a polypeptide, that initiates
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
 CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588
 CC -ADO03527 or ADO03530-ADO03559. Also included are using a transgenic
 CC plant to grow a progeny plant, an expression cassette (comprising a
 CC constitutive, inducible or tissue-specific promoter and a recombinant
 CC polynucleotide described above), a host cell comprising the expression
 CC cassette, producing a modified plant having a modified trait, identifying
 CC a factor that is modulated by or interacts with a polypeptide encoded by
 CC the polynucleotide sequence and identifying at least one downstream
 CC polynucleotide sequence that is subject to a regulatory effect of any of
 CC the polypeptides encoded by the polynucleotide described above. The
 CC transgenic plant is useful for producing a plant that has an altered
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to
 CC salt, tolerance to phosphate limitation, tolerance to potassium
 CC limitation, decreased sensitivity to nitrogen limitation), altered
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered
 CC response to ethylene, disease resistance, altered susceptibility to
 CC

CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to
 CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered
 CC susceptibility to Sclerotinia, altered sugar sensing, improved seed
 CC germination and seedling vigor, early flowering, late flowering, extended
 CC period of flowering, an inflorescence architectural change, a change in
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell
 CC differentiation, altered phyllotaxy, altered branching pattern, reduced
 CC apical dominance, reduced trichome density, ectopic trichome development,
 CC altered trichome development, altered stem morphology, increased root
 CC growth, increased root hairs, altered seed development, altered cell
 CC proliferation/cell differentiation, premature senescence, delayed
 CC senescence, lethality, increased necrosis, an increase in seedling or
 CC plant size, decreased plant size, a change in leaf morphology, increased
 CC altered leaf development, increased leaf size and mass, glossy leaves,
 CC leaf cell expansion, change in seed morphology, altered seed coloration,
 CC increased seed size, decreased seed size, altered seed shape, change in
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenly lipid
 CC content, increased leaf anthocyanins, an alteration of leaf fatty acid
 CC content, an alteration of leaf glucosinolate content, change in seed
 CC biochemistry, an increase in seed oil content, decrease in seed oil
 CC content, increase in seed fatty acid content, decrease in seed fatty acid
 CC content, increase in seed protein content, decrease in seed protein
 CC content, alteration in seed prenly lipid content, increase in seed
 CC sterols, upregulation of genes involved in secondary metabolism, increase
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in
 CC light response or shade avoidance. The present sequence encodes an
 CC orthologue of a thalacress transcription factor isolated from Corn.
 XX
 SQ Sequence 823 BP; 172 A; 258 C; 247 G; 144 T; 0 U; 2 Other;
 Alignment Scores:
 Pred. No.: 1,42e-26 Length: 823
 Score: 249.00 Matches: 44
 Percent Similarity: 88.89% Conservative: 4
 Best Local Similarity: 81.48% Mismatches: 6
 Query Match: 83.56% Indels: 0
 DB: 12 Gaps: 0
 US-10-666-642-194_COPY_111_164 (1-54) x ADO03201 (1-823)
 Qy 1 AspGlyPheLysTrpArgLysTyrgLysLysSerValLysAsnAsnIleAsnLysArg 20
 Db 441 GACGGATTCAAGTGGAGGAGTACGGGAAGAAGGCGCTCAAGAACAGCCCAATCCAAAGG 500
 Qy 21 AsnTyTyTyLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
 Db 501 AACTACTACCCGCTGCTGCTGGAGGGCTGCGCGGTGAAGAAGCGGTGGAGAGGACCGC 560
 Qy 41 AspAspAlaAlaTyTyValIleThrTyrgLysValHis 54
 Db 561 GACGACCCCGCTAGCTCATCACCCACTACGACGGCGTCCAC 602
 RESULT 6
 ADO62507
 ID ADO62507 standard; DNA; 823 BP.
 XX ADO62507;
 AC ADO62507;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Transcription factor G1274 orthologous sequence, SEQ ID 974.
 XX
 KW Plant; transcription factor; transgenic plant; abiotic stress tolerance;
 KW osmotic stress tolerance; cold tolerance; heat tolerance;
 KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
 KW glyphosate resistance; flowering; fertility; seed development; ds.
 OS Zea mays.
 XX
 FN WO2004031349-A2.
 XX
 PD 15-APR-2004.

XX 18-SEP-2003; 2003WO-US030292.
 XX 18-SEP-2002; 2002US-0411837P.
 XX 17-DEC-2002; 2002US-0434166P.
 XX 24-APR-2003; 2003US-045809P.
 XX (MEND-) MENDEL BIOTECHNOLOGY INC.
 XX Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;
 PI Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK;
 XX WPI; 2004-330163/30.
 XX New recombinant polynucleotide encoding transcription factor
 PT polypeptides, useful for producing transgenic plants with advantageous
 PT properties compared to a reference plant.
 XX Claim 1; SEQ ID NO 974; 510pp; English.
 XX The present invention relates to novel plant transcription factor
 CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
 CC sequences can be used to produce transgenic plants, which overexpress
 CC (II), where the transgenic plant has an altered trait as compared to a
 CC non-transgenic plant or wild-type plant. The transgenic plant comprises
 CC an altered trait selected from increased tolerance to abiotic stress,
 CC increased tolerance to osmotic stress, increased tolerance to cold,
 CC increased germination in cold, increased tolerance to heat, increased
 CC germination in heat, increased tolerance to freezing conditions,
 CC increased tolerance to low nitrogen conditions, increased tolerance to
 CC low phosphate conditions, increased tolerance to disease, including
 CC fungal disease and particularly Bysiphe, Fusarium and Botrytis,
 CC increased tolerance to multiple fungal pathogens, increased resistance to
 CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
 CC increased sensitivity to ACC, altered sugar sensing, increased tolerance
 CC to sugars, altered carbon/nitrogen sensing, early flowering, late
 CC flowering, altered flower structure, loss of flower determinacy, reduced
 CC fertility, altered shoot meristem development, altered branching pattern,
 CC altered stem morphology, altered vascular tissue structure, reduced
 CC apical dominance, altered trichome density, altered trichome development,
 CC altered trichome structure, altered root development, altered shade
 CC avoidance, altered seed development, altered seed ripening, altered seed
 CC germination, slow growth, fast growth, altered cell differentiation,
 CC altered cell proliferation, altered cell expansion, altered phase change,
 CC altered senescence, abnormal embryo development, altered programmed cell
 CC death, lethality when overexpressed, altered necrosis patterns, increased
 CC plant size, increased biomass, large seedlings, dwarfed plants, dark
 CC green leaves, change in leaf shape, increased leaf size and mass, light
 CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
 CC altered seed coloration, altered seed size, altered seed shape, large
 CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil
 CC content, altered seed protein content, altered seedprenyl content,
 CC altered leaf prenyl lipid content, increased anthocyanin levels, and
 CC decreased anthocyanin levels. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 823 BP; 172 A; 258 C; 247 G; 144 T; 0 U; 2 Other;
 Alignment Scores:
 Pred. No.: 1.42e-26 Length: 823
 Score: 249.00 Matches: 44
 Percent Similarity: 88.99% Conservative: 4
 Best Local Similarity: 81.48% Mismatches: 6
 Query Match: 83.56% Indels: 0
 DB: 12 Gaps: 0
 US-10-666-642-194_COPY_111_164 (1-54) x ADO62507 (1-823)
 Qy 1 AspGlyPheLysTyrArgLysTyrGlyLysSerValLysArgValGluArgAspGly 20
 Db 441 GACGGATTCAAGTGAGGAGTAGTCGGGAAGAGCGGCTCAAGAACAGCCCAATCCAAGG 500

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
 Db 501 AACTACTACCGCTGCTCGTGGAGGGCTGGCGCTGAAGAAGCGGTGGAGAGGACCGC 560
 Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
 Db 561 GACGAGCCCGCTACGTACGTATCACCACCTACGACGGCGTCCAC 602

RESULT 7
 ADI43068
 ID ADI43068 standard; DNA; 1663 BP.
 XX ADI43068;
 AC ADI43068;
 XX 22-APR-2004 (first entry)
 DT 22-APR-2004 (first entry)
 XX Plant transcription factor polynucleotide #1006.
 DE Plant transcription factor polynucleotide #1006.
 XX transgenic; plant; enhanced tolerance to abiotic stress;
 KW glyphosate tolerance; hormone sensitivity; disease resistance;
 KW sugar sensing; flowering; flower structure; stem bifurcation;
 KW branching pattern; apical dominance; trichome; stem morphology;
 KW root growth; root hair; seed development; cell proliferation;
 KW cell differentiation; premature senescence; necrosis; plant size;
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;
 KW transcription factor; gene; ds.
 XX Zea mays.
 OS Zea mays.
 XX US2004019927-A1.
 PN US2004019927-A1.
 XX 29-JAN-2004.
 PD 29-JAN-2004.
 XX 25-FEB-2003; 2003US-00374780.
 PF 25-FEB-2003; 2003US-00374780.
 XX 18-APR-2001; 2001US-00837944.
 PR 18-APR-2001; 2001US-00837944.
 PA (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMANN J L.
 PA (JIANG/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HAAK/) HAAKE V.
 PA (CREE/) CREELMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P E.
 PA (PILG/) PILGRIM M L.
 PA (DUBE/) DUBELL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 XX Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;
 PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;
 PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
 XX WPI; 2004-132245/13.
 DR WPI; 2004-132245/13.
 XX New transgenic plant comprising a recombinant polynucleotide of any one
 PT of more than 500 nucleotide sequences, useful in bioinformatic search
 PT methods.
 XX Claim 1; SEQ ID NO 1531; 435pp; English.
 PS Claim 1; SEQ ID NO 1531; 435pp; English.
 CC The invention describes a transgenic plant comprising a recombinant
 CC polynucleotide of any one of more than 500 nucleotide sequences fully
 CC defined in the specification or its complement. The method of the
 CC invention can be used to produce a plant having altered traits such as:
 CC enhanced tolerance to abiotic stress; glyphosate tolerance; hormone
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;

CC altered flower structure, change in stem bifurcations, altered branching
 CC pattern, reduced apical dominance, reduced trichome density; lack of
 CC trichomes; reduced ectopic trichome development; altered trichome
 CC development; increase in trichome number; altered stem morphology;
 CC increased root growth; increased root hairs; altered seed development;
 CC altered cell proliferation or cell differentiation; rapid development;
 CC premature senescence; increased necrosis; increase in seedling or plant
 CC size; decreased plant size; leaf morphology; seed morphology; seed
 CC biochemistry; increase in root anthocyanins; increase in plant
 CC anthocyanins, or alteration in light response or shade avoidance. The
 CC transgenic plant, polynucleotides and polypeptides are useful in
 CC bioinformatic search methods. This sequence represents a plant
 CC transcription factor, and an orthologue of Arabidopsis thaliana
 CC transcription factors isolated in the invention, that can be used in the
 CC creation of a transgenic plant with altered traits.

XX SQ Sequence 1663 BP; 417 A; 453 C; 494 G; 299 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3 6e-26	Length:	1663
Score:	249.00	Matches:	44
Percent Similarity:	88.8%	Conservative:	4
Best Local Similarity:	81.4%	Mismatches:	6
Query Match:	83.56%	Indels:	0
DB:	12	Gaps:	0

US-10-666-642-194_COPY_111_164 (1-54) x ADI43068 (1-1663)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20
 |||||
 1078 GACGGATTCACTGGAGGAAGTACGGGAAGAGCGCTGCAAGACAGCCCAATCCAAGG 1137
 |||||
 QY 21 AsnTyrLysCysSerSerGluGlyCysSerValLysLysValGluArgAspGly 40
 |||||
 DB 1138 AACTACTACCGCTGCTGTCGGAGGCGCTGCGCGTGAAGAACGGGTGGAGAGGACCGC 1197
 |||||
 QY 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
 |||||
 DB 1198 GACGACCCCGCTACGTCATCATCACCTACGACGCGGTCCAC 1239
 |||||

RESULT 8

AD003208
 ID AD003208 standard; cDNA; 1663 BP.
 XX AC AD003208;
 XX DT 01-JUL-2004 (first entry)
 XX DE Corn orthologue of Thalecress transcription factor, cDNA #183.
 KW Corn: transcription factor; ss; gene; plant; transgenic; abiotic stress;
 KW cold tolerance; heat tolerance; drought; osmotic stress;
 KW phosphate limitation; potassium limitation; nitrogen limitation;
 KW hormone sensitivity; disease resistance; sugar sensing; seed germination;
 KW flowering; inflorescence architectural change;
 KW meristem cell differentiation; phyllotaxy; apical dominance;
 KW trichome development; seed development; premature senescence;
 KW delayed senescence; lethality; necrosis; plant size; leaf morphology;
 KW seed morphology; secondary metabolism; light response; shade avoidance.
 OS Zea mays.
 XX PN US2004045049-A1.
 XX PD 04-MAR-2004.
 XX PF 10-APR-2003; 2003US-00412699.
 XX PR 13-SEP-1999; 99US-00394519.
 XX PR 21-JAN-2000; 2000US-00489376.
 XX PR 17-FEB-2000; 2000US-00506720.
 XX PR 22-MAR-2000; 2000US-00532591.
 XX PR 22-MAR-2000; 2000US-00533029.

PR 22-MAR-2000; 2000US-00533030.
 PR 22-MAR-2000; 2000US-00533392.
 PR 22-MAR-2000; 2000US-00533648.
 PR 06-APR-2000; 2000WO-US009448.
 PR 16-NOV-2000; 2000US-00713994.
 PR 27-MAR-2001; 2001US-00819142.
 PR 17-APR-2001; 2001US-00837444.
 PR 30-JAN-2002; 2002US-00958131.
 PR 14-JUN-2002; 2002US-00171468.
 PR 09-AUG-2002; 2002US-00225066.
 PR 09-AUG-2002; 2002US-00225067.
 PR 17-DEC-2002; 2002US-00225068.
 PR 25-FEB-2003; 2003US-0434166P.
 XX ZHAN// ZHANG J.
 PA (FROM//) FROMM M E.
 PA (HEAR//) HEARD J E.
 PA (RIEC//) RIECHMANN J L.
 PA (ADAM//) ADAM L J.
 PA (BROU//) BROUN P E.
 PA (PINE//) PINEDA O.
 PA (REUB//) REUBER T L.
 PA (KEDD//) KEDDIE J S.
 PA (YUGG//) YU G.
 PA (JIAN//) JIANG C.
 PA (SAMA//) SAMAHA R S.
 PA (PILG//) PILGRIM M L.
 PA (CREE//) CREELMAN R A.
 PA (DUBE//) DUBELL A N.
 PA (RATC//) RATCLIFFE O.
 PA (KUMI//) KUMIMOTO R.
 PA (SHER//) SHERMAN B K.
 XX Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE;
 PI Pineda O, Reuber TU, Keddie JS, Yu G, Jiang C, Samaha RS;
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
 PI Sherman BK;
 DR WPI; 2004-225755/21.
 XX New transgenic plant, useful in developing phenotypes with altered or
 PT improved characteristics or traits.
 PS Claim 1; SEQ ID NO 1622; 213pp; English.
 CC The invention relates to a transgenic plant comprises a recombinant
 CC polynucleotide having a polynucleotide sequence or its complementary
 CC sequence comprising a sequence encoding a polypeptide, that initiates
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
 CC Rice, Rape or Corn, comprising any of the sequences appearing as AD001588
 CC -AD003527 or AD003530-AD003559. Also included are using a transgenic
 CC plant to grow a progeny plant, an expression cassette (comprising a
 CC constitutive, inducible or tissue-specific promoter and a recombinant
 CC polynucleotide described above), a host cell comprising the expression
 CC cassette, producing a modified plant having a modified trait, identifying
 CC a factor that is modulated by or interacts with a polypeptide encoded by
 CC the polynucleotide sequence and identifying at least one downstream
 CC polynucleotide sequence that is subject to a regulatory effect of any of
 CC the polypeptides encoded by the polynucleotide described above. The
 CC transgenic plant is useful for producing a plant that has an altered
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to
 CC salt, tolerance to phosphate limitation, tolerance to potassium
 CC limitation, decreased sensitivity to nitrogen limitation), altered
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered
 CC response to ethylene, disease resistance, altered susceptibility to
 CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to
 CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered
 CC susceptibility to Sclerotinia, altered sugar sensing, improved seed
 CC germination and seedling vigor, early flowering, late flowering, extended
 CC period of flowering, an inflorescence architectural change, a change in

CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell
 CC differentiation, altered phyllotaxy, altered branching pattern, reduced
 CC apical dominance, reduced trichome density, ectopic trichome development,
 CC altered trichome development, altered stem morphology, increased root
 CC growth, increased root hairs, altered seed morphology, altered cell
 CC proliferation/cell differentiation, premature senescence, delayed
 CC senescence, lethality, increased necrosis, an increase in seedling or
 CC plant size, decreased plant size, a change in leaf morphology, increased
 CC altered leaf development, increased leaf size and mass, glossy leaves,
 CC leaf cell expansion, change in seed morphology, altered seed coloration,
 CC increased seed size, decreased seed size, altered seed shape, change in
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid
 CC content, increased leaf insoluble sugars, decreased leaf insoluble
 CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid
 CC content, an alteration of leaf glucosinolate content, change in seed
 CC biochemistry, an increase in seed oil content, decrease in seed oil
 CC content, increase in seed fatty acid content, decrease in seed fatty acid
 CC content, increase in seed protein content, decrease in seed protein
 CC content, alteration in seed prenyl lipid content, increase in seed
 CC sterols, upregulation of genes involved in secondary metabolism, increase
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in
 CC light response or shade avoidance. The present sequence encodes an
 CC orthologue of a thalecress transcription factor isolated from *Corn*.
 XX
 SQ Sequence 1663 BP; 417 A; 453 C; 494 G; 299 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3.6e-26 Length: 1663
 Score: 249.00 Matches: 44
 Percent Similarity: 88.89% Conservative: 4
 Best Local Similarity: 81.48% Mismatches: 6
 Query Match: 83.56% Indels: 0
 DB: 12 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x ADO03208 (1-1663)

Qy 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnLysArg 20
 Db 1078 GACGGATTCAAGTGGAGAGTACGGGAAGAGCGGTCAAGAACACGCCAATCCAAAGG 1137
 Qy 21 AsnTyrTrpLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
 Db 1138 AACTACTACCGCTGCTCGTGGAGGCGTGGCGGGAAGAGCGGTGAGAGGAGCGACCGC 1197
 Qy 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
 Db 1198 GACGACCCCGCTAGCTCATCACCACTACGACGGGCTCCAC 1239

RESULT 9

ADO03200
 ID ADO03200 standard; cDNA; 680 BP.

XX AC ADO03200;

XX DT 01-JUL-2004 (first entry)

XX DE Corn orthologue of Thalecress transcription factor, cDNA #179.

XX KW Corn; transcription factor; ss; gene; plant; transgenic; abiotic stress;
 KW cold tolerance; heat tolerance; drought; osmotic stress;
 KW phosphate limitation; potassium limitation; nitrogen limitation;
 KW hormone sensitivity; disease resistance; sugar sensing; seed germination;
 KW flowering; inflorescence architectural change;
 KW meristem cell differentiation; phyllotaxy; apical dominance;
 KW trichome development; seed development; premature senescence;
 KW delayed senescence; lethality; necrosis; plant size; leaf morphology;
 KW seed morphology; secondary metabolism; light response; shade avoidance.

XX OS Zea mays.

PN US2004045049-A1.

XX XX 04-MAR-2004.

XX 10-APR-2003; 2003US-00412699.
 XX 13-SEP-1999; 99US-00394519.
 PR 21-JAN-2000; 2000US-00489376.
 PR 17-FEB-2000; 2000US-00506720.
 PR 22-MAR-2000; 2000US-00532591.
 PR 22-MAR-2000; 2000US-00533029.
 PR 22-MAR-2000; 2000US-00533030.
 PR 22-MAR-2000; 2000US-00533392.
 PR 06-APR-2000; 2000US-00533648.
 PR 16-NOV-2000; 2000WO-US009448.
 PR 17-MAR-2001; 2001US-00819142.
 PR 17-APR-2001; 2001US-00837444.
 PR 30-JAN-2002; 2002US-00958131.
 PR 14-JUN-2002; 2002US-00171468.
 PR 09-AUG-2002; 2002US-00225066.
 PR 09-AUG-2002; 2002US-00225067.
 PR 09-AUG-2002; 2002US-00225068.
 PR 17-DEC-2002; 2002US-0434166P.
 PR 25-FEB-2003; 2003US-00374780.

XX (ZHAN/) ZHANG J.
 PA (FROM/) FROMM M E.
 PA (HEAR/) HEARD J E.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUN P E.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMAHA R S.
 PA (PILG/) PILGRIM M L.
 PA (CREE/) CREELMAN R A.
 PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KUMI/) KUMIMOTO R.
 PA (SHER/) SHERMAN B K.

XX Zhang J, Fromm MB, Heard JB, Riechmann JL, Adam LJ, Broun PE;
 PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS;
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
 PI Sherman BK;

XX WPI: 2004-225755/21.

XX New transgenic plant, useful in developing phenotypes with altered or
 improved characteristics or traits.

XX Claim 1; SEQ ID NO 1614; 213pp; English.

XX The invention relates to a transgenic plant comprises a recombinant
 CC polynucleotide having a polynucleotide sequence or its complementary
 CC sequence comprising a sequence encoding a polypeptide, that initiates
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
 CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588
 CC -ADO03527 or ADO0330-ADO03559. Also included are using a transgenic
 CC plant to grow a progeny plant, an expression cassette (comprising a
 CC constitutive, inducible or tissue-specific promoter and a recombinant
 CC polynucleotide described above), a host cell comprising the expression
 CC cassette, producing a modified plant having a modified trait, identifying
 CC a factor that is modulated by or interacts with a polypeptide encoded by
 CC the polynucleotide sequence and identifying at least one downstream
 CC polynucleotide sequence that is subject to a regulatory effect of any of
 CC the polypeptides encoded by the polynucleotide described above. The
 CC transgenic plant is useful for producing a plant that has an altered
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to
 CC salt, tolerance to phosphate limitation, tolerance to potassium

CC limitation, decreased sensitivity to nitrogen limitation), altered
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered
 CC response to ethylene, disease resistance, altered susceptibility to
 CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to
 CC Bryopsis, altered susceptibility to Pseudomonas syringae, altered
 CC susceptibility to Scierotinia, altered sugar sensing, improved seed
 CC germination and seedling vigor, early flowering, late flowering, extended
 CC period of flowering, an inflorescence architectural change, a change in
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell
 CC differentiation, altered phylloclax, altered branching pattern, reduced
 CC apical dominance, reduced trichome density, ectopic trichome development,
 CC altered trichome development, altered stem morphology, increased root
 CC growth, increased root hairs, altered seed morphology, altered cell
 CC proliferation/cell differentiation, premature senescence, delayed
 CC senescence, lethality, increased necrosis, an increase in seedling or
 CC plant size, decreased plant size, a change in leaf morphology, increased
 CC altered leaf development, increased leaf size and mass, glossy leaves,
 CC leaf cell expansion, change in seed morphology, altered seed coloration,
 CC increased seed size, decreased seed size, altered seed shape, change in
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid
 CC content, increased leaf insoluble sugars, decreased leaf insoluble
 CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid
 CC content, an alteration of leaf glucosinolate content, change in seed
 CC biochemistry, an increase in seed oil content, decrease in seed oil
 CC content, increase in seed fatty acid content, decrease in seed fatty acid
 CC content, increase in seed protein content, decrease in seed protein
 CC content, alteration in seed prenyl lipid content, increase in seed
 CC sterols, upregulation of genes involved in secondary metabolism, increase
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in
 CC light response or shade avoidance. The present sequence encodes an
 CC orthologue of a thalacress transcription factor isolated from Corn.
 XX
 SQ Sequence 680 BP; 129 A; 206 C; 213 G; 132 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: Length: 680
 Score: 248.00 Matches: 42
 Percent Similarity: 92.59% Conservative: 8
 Best Local Similarity: 77.78% Mismatches: 4
 Query Match: 83.22% Indels: 0
 DB: 12 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x ADO03200 (1-680)

Qy 1 AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAsnIleAsnLysArg 20
 Db 57 GACGGCTACAGTGGAGGANGTACGCGAAGAGTCCGTCAAGAACGCCCCCAACCAAGG 116
 Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
 Db 117 AACTACTACCGGTGCTCGACGCGAAGGGTGCACGTGAGAACGGGTGGAGCGGCAAG 176
 Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
 Db 177 GACGACCCACGACTACGTGTGTCGACGACGTACGACGAGGGGATGCAC 218

RESULT 10

ADO62506

ID ADO62506 standard; DNA; 680 BP.

XX ADO62506;

XX 15-JUL-2004 (first entry)

XX Transcription factor G1274 orthologous sequence, SEQ ID 973.

XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;
 KW osmotic stress tolerance; cold tolerance; heat tolerance;
 KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
 KW glyphosate resistance; flowering; fertility; seed development; ds.
 XX
 OS Zea mays.

PN WO2004031349-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 18-SEP-2003; 2003WO-US030292.
 XX
 PR 18-SEP-2002; 2002US-0411837P.
 PR 17-DEC-2002; 2002US-0434166P.
 PR 24-APR-2003; 2003US-045809P.
 XX
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 XX
 PI Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;
 PI Riechmann JL, Haake V, Dubell AN, Keddle JS, Sherman BK;
 XX
 DR WPI; 2004-330163/30.
 XX
 PT New recombinant polynucleotide encoding transcription factor
 PT polypeptides, useful for producing transgenic plants with advantageous
 PT properties compared to a reference plant.
 XX
 PS Claim 1; SEQ ID NO 973; 510pp; English.
 XX

The present invention relates to novel plant transcription factor
 proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
 sequences can be used to produce transgenic plants, which overexpress
 (II), where the transgenic plant has an altered trait as compared to a
 non-transgenic plant or wild-type plant. The transgenic plant comprises
 an altered trait selected from increased tolerance to abiotic stress,
 increased tolerance to osmotic stress, increased tolerance to cold,
 increased germination in cold, increased tolerance to heat, increased
 germination in heat, increased tolerance to freezing conditions,
 increased tolerance to low nitrogen conditions, increased tolerance to
 low phosphate conditions, increased tolerance to disease, including
 fungal disease and particularly Erysiphe, Fusarium and Botrytis,
 increased tolerance to multiple fungal pathogens, increased resistance to
 glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
 increased sensitivity to ACC, altered sugar sensing, increased tolerance
 to sugars, altered carbon/nitrogen sensing, early flowering, late
 flowering, altered flower structure, loss of flower determinacy, reduced
 fertility, altered shoot meristem development, altered branching pattern,
 altered stem morphology, altered vascular tissue structure, reduced
 apical dominance, altered trichome density, altered trichome development,
 altered trichome structure, altered root development, altered shade
 avoidance, altered seed development, altered seed ripening, altered seed
 germination, slow growth, fast growth, altered cell differentiation,
 altered cell proliferation, altered cell expansion, altered phase change,
 altered senescence, abnormal embryo development, altered programmed cell
 death, lethality when overexpressed, altered necrosis patterns, increased
 plant size, increased biomass, large seedlings, dwarfed plants, dark
 green leaves, change in leaf shape, increased leaf size and mass, light
 green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
 altered seed coloration, altered seed size, altered seed shape, large
 seed, increased leaf wax, increased leaf fatty acids, altered seed oil
 content, altered seed protein content, altered seedprenyl content,
 altered leaf prenyl lipid content, increased anthocyanin levels, and
 decreased anthocyanin levels. Note: The sequence data for this patent did
 not form part of the printed specification, but was obtained in
 electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 680 BP; 129 A; 206 C; 213 G; 132 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: Length: 680
 Score: 248.00 Matches: 42
 Percent Similarity: 92.59% Conservative: 8
 Best Local Similarity: 77.78% Mismatches: 4
 Query Match: 83.22% Indels: 0
 DB: 12 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x ADO62506 (1-680)

Score: 248.00 Matches: 42
Percent Similarity: 92.59% Conservative: 8
Best Local Similarity: 77.78% Mismatches: 4
Query Match: 83.22% Indels: 0
DB: 12 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x ADO03199 (1-743)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20
DB 18 GACGGCTACAGTGGAGGAGTACGGCAAGAGTCCGTCAAGAACAGCCCCAACCCAAAGG 77

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysValGluArgAspGly 40
DB 78 AACTACTACCGTGTCTCGACGGAAGGGTCAACGTGAAGACGGGTGGAGCGGACAAAG 137

QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
DB 138 GACGACCCAGCTACGTGTGACGAGTACGAGGGGATGCAC 179

RESULT 12
ADO62505
ID ADO62505 standard; DNA; 743 BP.
XX AC ADO62505;
XX DT 15-JUL-2004 (first entry)
XX DE Transcription factor G1274 orthologous sequence, SEQ ID 972.
XX KW Plant; transcription factor; transgenic plant; abiotic stress tolerance;
KW osmotic stress tolerance; cold tolerance; heat tolerance;
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
KW glyphosate resistance; flowering; fertility; seed development; ds.
XX OS Zea mays.
XX PN WO2004031349-A2.
XX PD 15-APR-2004.
XX PF 18-SEP-2003; 2003WO-US030292.
XX PR 18-SEP-2002; 2002US-0411837P.
PR 17-DEC-2002; 2002US-0434166P.
PR 24-APR-2003; 2003US-0465809P.
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
XX PI Jiang C. Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;
PI Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK;
XX WPI; 2004-330163/30.
XX PT New recombinant polynucleotide encoding transcription factor
PT polypeptides, useful for producing transgenic plants with advantageous
PT properties compared to a reference plant.
XX PS Claim 1; SEQ ID NO 972; 510pp; English.
XX CC The present invention relates to novel plant transcription factor
CC sequences (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
CC proteins can be used to produce transgenic plants, which overexpress
CC (II), where the transgenic plant has an altered trait as compared to a
CC non-transgenic plant or wild-type plant. The transgenic plant comprises
CC an altered trait selected from increased tolerance to abiotic stresses,
CC increased tolerance to osmotic stress, increased tolerance to cold,
CC increased germination in cold, increased tolerance to heat, increased
CC germination in heat, increased tolerance to freezing conditions,
CC increased tolerance to low nitrogen conditions, increased tolerance to
CC low phosphate conditions, increased tolerance to disease, including
CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,
CC increased tolerance to multiple fungal pathogens, increased resistance to

CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
CC increased sensitivity to ACC, altered sugar sensing, increased tolerance
CC to sugars, altered carbon/nitrogen sensing, early flowering, late
CC flowering, altered flower structure, loss of flower determinacy, reduced
CC fertility, altered shoot meristem development, altered branching pattern,
CC altered stem morphology, altered vascular tissue structure, reduced
CC apical dominance, altered trichome density, altered trichome development,
CC altered trichome structure, altered root development, altered shade
CC avoidance, altered seed development, altered seed ripening, altered seed
CC germination, slow growth, fast growth, altered cell differentiation,
CC altered cell proliferation, altered cell expansion, altered phase change,
CC altered senescence, abnormal embryo development, altered programmed cell
CC death, lethality when overexpressed, altered necrosis patterns, increased
CC plant size, increased biomass, large seedlings, dwarfed plants, dark
CC green leaves, change in leaf shape, increased leaf size and mass, light
CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
CC altered seed coloration, altered seed size, altered seed shape, large
CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil
CC content, altered seed protein content, altered seedprenyl content,
CC altered leaf prenyl lipid content, increased anthocyanin levels, and
CC decreased anthocyanin levels. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 743 BP; 158 A; 210 C; 216 G; 159 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.73e-26 Length: 743
Score: 248.00 Matches: 42
Percent Similarity: 92.59% Conservative: 8
Best Local Similarity: 77.78% Mismatches: 4
Query Match: 83.22% Indels: 0
DB: 12 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x ADO62505 (1-743)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20
DB 18 GACGGCTACAGTGGAGGAGTACGGCAAGAGTCCGTCAAGAACAGCCCCAACCCAAAG 77

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysValGluArgAspGly 40
DB 78 AACTACTACCGTGTCTCGACGGAAGGGTCAACGTGAAGACGGGTGGAGCGGACAAAG 137

QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
DB 138 GACGACCCAGCTACGTGTGACGAGTACGAGGGGATGCAC 179

RESULT 13
ADO03196/c
ID ADO03196 standard; cDNA; 974 BP.
XX AC ADO03196;
XX DT 01-JUL-2004 (first entry)
XX DE Soybean orthologue of Thalecress transcription factor, cDNA #267.
XX KW Soybean; transcription factor; ss; gene; plant; transgenic;
KW abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;
KW phosphate limitation; potassium limitation; nitrogen limitation;
KW hormone sensitivity; disease resistance; sugar sensing; seed germination;
KW flowering; inflorescence architectural change;
KW meristem cell differentiation; phytoalexin; apical dominance;
KW trichome development; seed development; premature senescence;
KW delayed senescence; lethality; necrosis; plant size; leaf morphology;
KW seed morphology; secondary metabolism; light response; shade avoidance.
XX OS Glycine max.
XX PN US2004045049-A1.
XX

PD 04-MAR-2004.
 XX 10-APR-2003; 2003US-00412699.
 PR 13-SEP-1999; 99US-00394519.
 PR 21-JAN-2000; 2000US-00489376.
 PR 17-FEB-2000; 2000US-00506720.
 PR 22-MAR-2000; 2000US-00532591.
 PR 22-MAR-2000; 2000US-00533029.
 PR 22-MAR-2000; 2000US-00533030.
 PR 22-MAR-2000; 2000US-00533392.
 PR 22-MAR-2000; 2000US-00533648.
 PR 06-APR-2000; 2000WO-US009448.
 PR 16-NOV-2000; 2000US-00713994.
 PR 27-MAR-2001; 2001US-00819142.
 PR 30-JAN-2002; 2001US-00837444.
 PR 14-JUN-2002; 2002US-00171468.
 PR 09-AUG-2002; 2002US-00225066.
 PR 09-AUG-2002; 2002US-00225067.
 PR 09-AUG-2002; 2002US-00225068.
 PR 17-DEC-2002; 2002US-0434166P.
 PR 25-FEB-2003; 2003US-00374780.
 XX (ZHAN//) ZHANG J.
 PA (FROM//) FROMM M E.
 PA (HEAR//) HEARD J E.
 PA (RISC//) RIECHMANN J L.
 PA (ADAM//) ADAM L J.
 PA (BROU//) BROUN P E.
 PA (PINE//) PINEDA O.
 PA (REUB//) REUBER T L.
 PA (KEDD//) KEDDIE J S.
 PA (YUGG//) YU G.
 PA (JTAN//) JTANG C.
 PA (SAMA//) SAMAHA R S.
 PA (PILG//) PILGRIM M L.
 PA (CREE//) CREELMAN R A.
 PA (DUBE//) DUBELL A N.
 PA (RATC//) RATCLIFFE O.
 PA (KUMI//) KUMIMOTO R.
 PA (SHER//) SHERMAN B K.
 XX Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE;
 PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS;
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
 PI Sherman BK;
 XX WPI; 2004-225755/21.
 DR New transgenic plant, useful in developing phenotypes with altered or
 XX improved characteristics or traits.
 PT Claim 1; SEQ ID NO 1610; 213pp; English.
 PS The invention relates to a transgenic plant comprises a recombinant
 XX polynucleotide having a polynucleotide sequence or its complementary
 CC sequence comprising a sequence encoding a polypeptide, that initiates
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
 CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588
 CC -AD003527 or ADO03530-AD003559. Also included are using a transgenic
 CC plant to grow a progeny plant, an expression cassette (comprising a
 CC constitutive, inducible or tissue-specific promoter and a recombinant
 CC polynucleotide described above), a host cell comprising the expression
 CC cassette, producing a modified plant having a modified trait, identifying
 CC a factor that is modulated by or interacts with a polypeptide encoded by
 CC the polynucleotide sequence and identifying at least one downstream
 CC polynucleotide sequence that is subject to a regulatory effect of any of
 CC the polypeptides encoded by the polynucleotide described above. The
 CC transgenic plant is useful for producing a plant that has an altered
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to

CC salt, tolerance to phosphate limitation, tolerance to potassium
 CC limitation, decreased sensitivity to nitrogen limitation), altered
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered
 CC response to ethylene, disease resistance, altered susceptibility to
 CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to
 CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered
 CC susceptibility to Sclerotinia, altered sugar sensing, improved seed
 CC germination and seedling vigor, early flowering, late flowering, extended
 CC period of flowering, an inflorescence architectural change, a change in
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell
 CC differentiation, altered phyllotaxy, altered branching pattern, reduced
 CC apical dominance, reduced trichome density, ectopic trichome development,
 CC altered trichome development, altered stem morphology, increased root
 CC growth, increased root hairs, altered seed development, delayed cell
 CC proliferation/cell differentiation, premature senescence, delayed
 CC senescence, lethality, increased necrosis, an increase in seedling or
 CC plant size, decreased plant size, a change in leaf morphology, increased
 CC altered leaf development, increased leaf size and mass, glossy leaves,
 CC leaf cell expansion, change in seed morphology, altered seed coloration,
 CC increased seed size, decreased seed size, altered seed shape, change in
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid
 CC content, increased leaf insoluble sugars, decreased leaf insoluble
 CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid
 CC content, an alteration of leaf glucosinolate content, change in seed
 CC biochemistry, an increase in seed oil content, decrease in seed oil
 CC content, increase in seed fatty acid content, decrease in seed fatty acid
 CC content, increase in seed protein content, decrease in seed protein
 CC content, upregulation of genes involved in secondary metabolism, increase
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in
 CC light response or shade avoidance. The present sequence encodes an
 CC orthologue of a thalecress transcription factor isolated from Soybean.
 XX
 SQ Sequence 974 BP; 294 A; 177 C; 195 G; 308 T; 0 U; 0 Other;
 Alignment Scores: Length: 974
 Pred. No.: 3.48e-26 Matches: 45
 Score: 247.00 Conservative: 4
 Percent Similarity: 90.74% Mismatches: 5
 Best Local Similarity: 83.33% Indels: 0
 Query Match: 82.89% Gaps: 0
 DB: 12
 US-10-666-642-194_COPY_111_164 (1-54) x ADO03196 (1-974)
 Qy 1 AspGlyPheLysTyrArgLysTyrGlyLysLysSerVallysAsnAsnLysArg 20
 Db 582 GATGATACAGTGGAGGAGTACGGCAGAGAGTCCGTGAGAGCAGTCCCATCTAAGG 523
 Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerVallysLysArgValGluArgAspGly 40
 Db 522 AACTACTACAAATGTTCAAGTGGAGGATGCAGTGTGAAGAAAGGTTGGAAGGATAGA 463
 Qy 41 AspAspAlaalaTyrValIleThrThrTyrGluGlyValHis 54
 Db 462 GATGACTACAGCTACGTGATACCAACATATGAAGGTGTGCAC 421
 RESULT 14
 ADO62502/c
 ID ADO62502 standard; DNA; 974 BP.
 XX ADO62502;
 AC ADO62502;
 DT 15-JUL-2004 (first entry)
 XX Transcription factor G1274 orthologous sequence, SEQ ID 969.
 DE Plant; transcription factor; transgenic plant; abiotic stress tolerance;
 XX osmotic stress tolerance; cold tolerance; heat tolerance;
 KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
 KW glyphosate resistance; flowering; fertility; seed development; ds.
 XX Glycine max.
 OS

XX WO2004031349-A2.
 PN 15-APR-2004.
 PD
 XX 18-SEP-2003; 2003WO-US030292.
 PF
 XX 18-SEP-2002; 2002US-0411837P.
 PR 17-DEC-2002; 2002US-0434166P.
 PR 24-APR-2003; 2003US-0465809P.
 XX (MEND-) MENDEL BIOTECHNOLOGY INC.
 XX
 XX Jiang C. Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;
 PI Riechmann JL, Haake V, Dubell AN, Keddle JS, Sherman BK;
 XX WPI; 2004-330163/30.
 DR
 XX New recombinant polynucleotide encoding transcription factor
 PT polypeptides, useful for producing transgenic plants with advantageous
 PT properties compared to a reference plant.
 XX
 XX Claim 1; SEQ ID NO 969; 510pp; English.
 PS
 XX The present invention relates to novel plant transcription factor
 CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
 CC sequences can be used to produce transgenic plants, which overexpress
 CC (II), where the transgenic plant has an altered trait as compared to a
 CC non-transgenic plant or wild-type plant. The transgenic plant comprises
 CC an altered trait selected from increased tolerance to abiotic stresses,
 CC increased tolerance to osmotic stress, increased tolerance to cold,
 CC increased germination in cold, increased tolerance to heat, increased
 CC germination in heat, increased tolerance to freezing conditions.
 CC increased tolerance to low nitrogen conditions, increased tolerance to
 CC low phosphate conditions, increased tolerance to disease, including
 CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,
 CC increased tolerance to multiple fungal pathogens, increased resistance to
 CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
 CC increased sensitivity to ACC, altered sugar sensing, increased tolerance
 CC to sugars, altered carbon/nitrogen sensing, early flowering, late
 CC flowering, altered flower structure, loss of flower determinacy, reduced
 CC fertility, altered shoot meristem development, altered branching pattern,
 CC altered stem morphology, altered vascular tissue structure, reduced
 CC apical dominance, altered trichome density, altered trichome development,
 CC altered trichome structure, altered root development, altered shade
 CC avoidance, altered seed development, altered seed ripening, altered seed
 CC germination, slow growth, fast growth, altered cell differentiation,
 CC altered cell proliferation, altered cell expansion, altered phase change,
 CC altered senescence, abnormal embryo development, altered programmed cell
 CC death, lethality when overexpressed, altered necrosis patterns, increased
 CC plant size, increased biomass, large seedlings, dwarfed plants, dark
 CC green leaves, change in leaf shape, increased leaf size and mass, light
 CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
 CC altered seed coloration, altered seed size, altered seed shape, large
 CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil
 CC content, altered seed protein content, altered seedprenyl content,
 CC altered leaf prenyl lipid content, increased anthocyanin levels, and
 CC decreased anthocyanin levels. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 974 BP; 294 A; 177 C; 195 G; 308 T; 0 U; 0 Other;
 SQ

Alignment Scores:

Pred. No.:	3,48e-26	Length:	974
Score:	247.00	Matches:	45
Percent Similarity:	90.74%	Conservative:	4
Best Local Similarity:	83.33%	Mismatches:	5
Query Match:	82.89%	Indels:	0
DB:	12	Gaps:	0

US-10-666-642-194_COPY_111_164 (1-54) x ADO62502 (1-974)

QY 1 AspGlyPheLysTrpArgLysTrpGlyLysLysSerValLysAsnAsnLysArg 20
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 582 GATGATACAAAGTGGAGGAGTACGGCAGAGAGTCCGTGAAGAGCAGTCCCAATCAAGG 523
 QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 522 AACTACTACAAATGTTCAAGTGGAGGATGCAGTGTGAAGAAAGGTTGGAAGGATAGA 463
 QY 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 462 GATGACTACAGCTACGTGATACCAACATATGAGGTGTGCAC 421

RESULT 15

ADI43067

ID ADI43067 standard; DNA; 1696 BP.

XX

AC ADI43067;

XX

DT 22-APR-2004 (first entry)

XX

DE Plant transcription factor polynucleotide #1005.

XX

KW transgenic; plant; enhanced tolerance to abiotic stress;
 KW glyphosphate tolerance; hormone sensitivity; disease resistance;
 KW sugar sensing; flowering; flower structure; stem bifurcation;
 KW branching pattern; apical dominance; trichome; stem morphology;
 KW root growth; root hair; seed development; cell proliferation;
 KW cell differentiation; premature senescence; necrosis; plant size;
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;
 KW transcription factor; gene; ds.

OS Zea mays.

XX

XX US2004019927-A1.

PN

PD 29-JAN-2004.

XX

PF 25-FEB-2003; 2003US-00374780.

XX

PR 18-APR-2001; 2001US-00837944.

XX

PA (SHER/) SHERMAN B K.

PA (RIEC/) RIECHMANN J L.

PA (JIANG/) JIANG C.

PA (HEAR/) HEARD J E.

PA (HAAK/) HAAKE V.

PA (CREE/) CREELMAN R A.

PA (RATC/) RATCLIFFE O.

PA (ADAM/) ADAM L J.

PA (REUB/) REUBER T L.

PA (KEDD/) KEDDIE J.

PA (BROU/) BROUN P B.

PA (PILG/) PILGRIM M L.

PA (DUBE/) DUBELL A N.

PA (PINE/) PINEDA O.

PA (YUGG/) YU G.

XX

XX Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;

PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddle J, Broun PE;

PI Pilgrim ML, Dubell AN, Pineda O, Yu G;

XX

XX WPI; 2004-132245/13.

XX

XX New transgenic plant comprising a recombinant polynucleotide of any one
 PT of more than 500 nucleotide sequences, useful in bioinformatic search
 PT methods.
 XX
 XX Claim 1; SEQ ID NO 1530; 435pp; English.
 PS
 XX The invention describes a transgenic plant comprising a recombinant
 CC polynucleotide of any one of more than 500 nucleotide sequences fully

CC defined in the specification or its complement. The method of the
CC invention can be used to produced a plant having altered traits such as:
CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone
CC sensitivity; disease resistance; sugar sensing; early or late flowering;
CC altered flower structure, change in stem bifurcations, altered branching
CC pattern, reduced apical dominance, reduced trichome density; lack of
CC trichomes; reduced ectopic trichome development; altered trichome
CC development; increase in trichome number; altered stem morphology;
CC increased root growth; increased root hairs; altered seed development;
CC altered cell proliferation or cell differentiation; rapid development;
CC premature senescence; increased necrosis; increase in seedling or plant
CC size; decreased plant size; leaf morphology; seed morphology; seed
CC biochemistry; increase in root anthocyanins; increase in plant
CC anthocyanins, or alteration in light response or shade avoidance. The
CC transgenic plant, polynucleotides and polypeptides are useful in
CC bioinformatic search methods. This sequence represents a plant
CC transcription factor, and an orthologue of Arabidopsis thaliana
CC transcription factors isolated in the invention, that can be used in the
CC creation of a transgenic plant with altered traits.
XX

SQ Sequence 1696 BP; 433 A; 436 C; 407 G; 420 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2e-25	Length:	1696
Score:	244.00	Matches:	43
Percent Similarity:	88.89%	Conservative:	5
Best Local Similarity:	79.63%	Mismatches:	6
Query Match:	81.88%	Indels:	0
DB:	12	Gaps:	0

US-10-666-642-194_COPY_111_164 (1-54) x ADI43067 (1-1696)

Qy	1	AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAsnIleAsnLysArg	20
Db	394	GATGATTCAATCGAGGAGTATGCGCAAGAGGCTGTCAAGAGTAGCCCAATCCAAGG	453
Qy	21	AsnTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly	40
Db	454	AACTACTACCGCTGCTCGCGAGGGCTGCGCGGTGAAGAAGCGGTGGAGAGGACCGC	513
Qy	41	AspAspAlaIleTyrValIleThrTyrGluGlyValHis	54
Db	514	GACGACCCCGCTACGTATCACCACCTACGACGCGCTCCAC	555

Search completed: August 26, 2005, 00:18:37
Job time : 397 secs

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